## **SEARCH REQUEST FORM**

 Requestor's Name:
 Serial Number:
 Og / 462 955

 Date:
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 Phone:
 308 - 6043
 Art Unit:
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### Search Topic

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevent citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevent claim(s).

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Date completed: 6 Search Site **Vendors** Searcher: \_ S. S. L. C. Berry \_\_\_\_ IG Terminal time: \_\_\_\_7 \_\_ STN -Elapsed-time: \_\_\_\_ Pre-S \_\_\_\_ Dialog CPU time: Type of Search \_\_\_ APS Total time: \_\_\_ 7 N.A. Sequence \_\_ Geninfo Number of Searches: \_\_\_\_ A.A. Sequence \_\_\_\_ SDC Number of Databases: Structure \_\_\_ DARC/Questel Bibliographic Other Gomes /

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June 19, 2002, 15:43:14; Search time 5904.86 Seconds (without alignments) 70.879 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result Query
No. Score Match Length DB ID
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Description

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13	16.8	84			AB019552		ABO	19552	Aeropyrum
14 15	16.8	8 4			AB078015 AB078016		ABO	78015	Aeropyrum
16	16.8	84			AB078018		ABO	78018	Aeropyrum
17	16.8	8 4 4			AB078017 AB078022		ABO	78017	Aeropyrum
19	16.8	84			AB078019		ABO	78019	Aeropyrum
20	16.8	84			AB078021		ABO	78021	Aeropyrum
22	16.8	20 d			AB019554		ABO	19554	Aeropyrum
c 23	16.8	2.00			AE004743		ABO	04743	Aeropyrum
	16.8	84			AB008745		ABO	08745	Aeropyrum
c 25	16.8	84.	2		AP000062		APO	00062	Aeropyrum
27	16.4	8 6			AY011570 AY011571		AYO	11570	Procavia
28	16	80.			AX184404		AXI	84404	Sequence
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32	16	80.			MTCY2B12		AE0	0/014 011 M3	Mycobacte /cobacteri
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	·S	79.			AF227236		AF2	27236	Halobacte
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RESULT									
LOCUS					21 bp	DNA	linear	PAT	17-DEC-2001
DEFINITION		Sequence 7	from patent U	ater	s 6303345.				
VERSION		72776.1	GI	:17912267	29;				
SOURCE		Unknown.							
ORGANIS	_	41	ed.						
REFERENCE AUTHORS		<pre>1 (bases Rohde, W.,</pre>	1 to 21) Becker, D.	~ .	3	Hehn,A.	and Sala	Salamini,	Α,
TITLE		· 🖆	virus DNA		promoter			•	
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PLN 29-OCT-1996
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Citrus ichangensis satellite DNA.
x51946
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DPKRNILLLDVPRCNIEYLNYALLECVKNRAFSSDKYEPLSYIGFDHVHLVFRANVLPD
YLKISPDRIKLWNI"
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Coconut foliar decay virus DNA, clones NMORG, pORG, and pORGSAU3A.
Coconut foliar decay virus
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Rohde,W., Randles,J.W., Langridge,P. and Hanold,D.
Nucleotide sequence of a circular single-stranded DNA associated
with coconut foliar decay virus
Virology 176, 648-651 (1990)
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       Gaps
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Draft entry and printed sequence for [1] kindly submitted by W.Rhode, 15-MAR-1989, for release after publication.
Location/Qualifiers
                                                                                                                                                                                                                                                                                            1 (bases 1 to 1291)
Rohde,W., Becker,D., Randles,J.W., Hehn,A. and Salamini,F.
Use of a virus DNA as promoter
Patent: US 6303345-A 1 16-OCT-2001;
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103. .975
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Sequence 1 from patent US 6303345.
AR172770
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M29963.1 GI:323306
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                             ORIGIN
                                                                                                                                                                                                                                                                       SOURCE
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                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.

1 (bases 1 to 20400)
Canaday,J., Tessier,L.H., Imbault,P. and Paulus,F.
Analysis of Euglena gracilis alpha-, beta- and gamma-tubulin genes:
Introns and pre-mRNA maturation
Mol. Genet. Genomics 265 (1), 153-160 (2001)
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                                                                                                                                                                                                                                                       PLN 02-MAY-2001
                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                              Euglena gracilis gamma-tubulin gene, exons 1-14 sequence.
AF271736
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0
                                                                                                                      Score 17.4; DB 8; Length 181;
Pred. No. 7.6e+03;
                                                                                                                                             1; Indels
/organism="Citrus ichangensis"
/db_xref="taxon:2709"
/tissue_type="leaves"
1. .181
                                                                                                                                                                                                                                                       DNA
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                                                                                                                                           0; Mismatches
                                                                       23
                                                                                                                                                                                                                                                     20400 bp
                                                          /note="satellite DNA"
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814. .869
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Paulus, F.P. and Tessier, L.H.
Direct Submission
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19559...or
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/number=3
10800. .10913
/number=4
11103. .11171
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                                                                                                                   ch 87.0%;
1 Similarity 94.7%;
18; Conservative
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/number=2
9340. .9393
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/number=1
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17219. .17
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14064. .14
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Euglena gracilis
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                                                                                                                                 Best Local Similarity
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/db_xref="taxon:3039"
join(AF271738.1:1576 .1631,5406. .5518,6546. .6599,
join(AF271738.1:1576 .1631,5406. .5518,6546. .6599,
8036. .81449,8339. .8407,9728. .9807,10965. .1109.
11366. .11452,12006. .12092,14512. .14661,14769. .14840,
15074. .15148,15563. .15630,16802. .16895,17682. .17726,
19844. .19894,20816. .21040)
join(AF271738.1:1583. .1631,5406. .5518,6546. .6599,
8036. .8149,8339. .8407,9728. .9807,10965. .11010,
11366. .11452,12006. .12092,14512. .14661,14769. .14840,
15074. .12148,15563. .15630,16802. .16895,17682. .17726,
19824. .19894,20826. .20937)
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1 (bases 1 to 21040)
Canaday,J., Tessier,L.H., Imbault,P. and Paulus,F.
Analysis of Euglena gracilis alpha-, beta- and gamma-tubulin genes:
Introns and pre-mRNA maturation
Mol. Genet. Genomics 265 (1), 153-160 (2001)
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Paulus,F.P. and Tessler,L.H.
Direct Submission
Submitted (24-MAY-2000) IBMP, CNRS, 12 rue du General Zimmer,
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                                                                                                                                                                                                                                                              Length 20400;
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87.0%; Score 17.4; DB 8;
Best Local Similarity 94.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 1;
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/strain="Klebs 2"
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/protein_id="AAK37967.1"
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Location/Qualifiers
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/number=14
4729 c
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/number=5
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Euglena gracilis
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/translation="GNPMSAVERQQSHLARKKETHKEMRVYVTSEIKDEFRRMCEAQG
VTQSEMIEKLIKDAVSQHKGFVKD"
complement(326..414)
/gene="copA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mosaic plasmids and mosaic replicons: evolutionary lessons from the analysis of genetic diversity in IncFII-related replicons Microbiology 146 (Pt 9), 2267-2275 (2000)
ALTARISTATION="MAPPSAPILEQAPGEVGPPRRRCRRPRALKFADVAVYFSSEEWG
RILRPAQRTLYRDVMRETYGLIGALGCAGPKPALITWLERNIDDWEPAALDPGEYRRWY
TYPOKRTRYROKNEEKEVPPPRDYPRKOKRGRRKPSKPALIAPGYSGGPTCDPGCGTFPD
LPALESHKCAONLKKPYPCPDCGRRFSYPSLLVSHRRAHSGECPYVDQCGKRFSORK
NLSQHOYITHGERPYHCPDCGRRFSRSLAHNRTTHTGEKPHQCPSCGRRFSORL
ATHQRTHTGEKPYTCLECSRRFRQRTALVIHQRIHTGEKPYPCPDGERRFSSSRLVS
HRRVHSGERPYACHGRFRFQRFTLLQHQLLHTGEKPYPCDCGRRFSSSSRLVS
STHTEEKLHACDDCGRRFAYPSLLASHRVHSGERPYACDLCSKRFAQHGLL
HTGEKPRPCLECGRFRAYPSLLASHRVHSGERPYACDLCSKRFAQHQLL
HTGEKPPPCLECGRFRAYPSLLASHRVHSGERPYACDLCSKRFAQHQLL
ATGEKPRPCLECGRFRAYPSLLASHRVHSGERPYACDLCSKRFAQHQLL
ATGEKPRPCLECGRFRANSLAVHKCPNTHNGSPRPLIGGPNQRSSAL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (31-JUL-1998) Osborn A.M., Division of Microbiology, GBF, Division of Microbiology, GBF, Mascheroder Weg 1, Braunschweig, D-38124, GERMANY See also 211775.
                                                                                                                                                                                                                                                                                                                                                                                                                                                BCT 26-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   copB gene; orik gene; plasmid; repA gene; tapA gene; TerRleft gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Osborn, A. M., da Silva Tatley, F. M., Steyn, L. M., Pickup, R. W. and Saunders, J. R.
                                                                                                                                                                                                                                                                                                                                                                                                                   3830 bp DNA linear BCT 26-SEF ALOBSHella pneumoniae plasmid pGSH500 alpha replicon, partial. ALOB980 ALOB980. GI:4138114
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/organism="Klebsiella pneumoniae"
/plasmid="pGSH500"
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/protein_id="CAA08923.1"
/db_xref="G1:4138115"
/db_xref="SPTREMBL:09ZEW7"
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/transl_table=11
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432. .509
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Klebsiella pneumoniae
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Osborn, A.M.
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1 (bases 1 to 3830)
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Best Local Similarity 100.C
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KPN9980
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Shili,K., Arakli,R. and Nawa,H.
Direct Submission
Submitted (15-JUN-2000) Department of Molecular Neurobiology, Brain
Research Institute, Niigata University, asahimachi-dori 1-757,
Niigata 951-8885, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ishli,K., Araki,K. and Nawa,H. Cloning and characterization of a novel transcription factor HIT-39
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/protein_id="AAG53888.1"
/db_xref="G1:12483904"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.0%; Score 17.4; DB 8;
94.7%; Pred. No. 1.6e+03;
iive 0; Mismatches 1;
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/db_xref="taxon:10116"
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268. .1770
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10965. .11010
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Best Local Similarity 94.7%
Matches 18; Conservative
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Alsbrooks, 1 (Dases 1 to 31948)

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Rattus norvegicus clone CH230-5B20, *** SEQUENCING IN PROGRESS ***,
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Submitted (15-SBP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
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                                                                                          85.0%; Score 17; DB 1; Length 3830;
100.0%; Pred. No. 4e+03;
ive 0; Mismatches 0; Indels
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HTG; HTGS_PHASE1.
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CRLATESKSGNLSITRATRALKFLAELGLITYQTEYDPQIGCNIPTDITFTPALFSAL
DVSEVAVVAARRSRVEWENKQRKKQKLKPLEMDELIAKAWRFVRERFRSYQSERKSHG
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LYTABASHION="EFFISRCRDNOKFFRLITTLKRSASDRCHEDWLAVFTVDEIGLL
LVSFTLPFRFAISKLANPFYVLFRFRHPAAGCCLNPGINGWRFIPPPWRVTPVNRIEL
OLFVAFAGKLHPGIRGDVIATDGFRVVGNISIGFIGEERKILFPRHRLRKTSAHGYLO
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/translation="MFKPLWQHGRAICFADGWFEWKREGDKKQPYFIHRKDGQPILMA
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IAADGAVSADHFIWHPVTRAVGNVKNQGPELIEPVG"
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                                                                                                                                                                                                                                          /db_xref="SPTREMBL:Q9ZEW6"
/translation="MLRKLQAQFLCHWLLLCNISAVGCD"
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                                                                                                                                                                                                                                                                                                                                                                                                           'function="Replication protein"
                                                                               /function="antisense control"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="G1:4138117"
/db_xref="SPTREMBL:Q9ZEW5"
                                                                                                                                                                                       /protein_id="CAA08924.1"
/db_xref="GI:4138116"
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/db_xref="GI:4138118"
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/protein_id="CAA08927.1"
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/gene="TerRleft"
complement(1823, 1845)
/gene="TerRleft"
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/gene="TerRright"
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1535. .1719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'product="RepA"
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/538. 15:38
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/gene="tapA"
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/gene="oriR"
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/gene="oriR"
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2558. .2974
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                                                                                                                                                                                                                                     * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 20 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                   Consensus quality: 26514 bases at least Q40
Consensus quality: 29112 bases at least Q30
Consensus quality: 31138 bases at least Q20
Estimated insert size: 15885; sum-of-contigs estimation
Quality coverage: Ox in Q20 bases; agarose-fp estimation
Quality coverage: O.2x in Q20 bases; sum-of-contigs estimation
                                                                                                                  ------- Summary Statistics
Assembly program: Phrap; version 0.990329First call to
  2001 this sequence version replaced gi:17062140
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                                                  Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
               Center: Baylor College of Medicine
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/organism="Rattus norvegicus" /db\_xref="taxon:10116" /clone="CH230-5B20"

source

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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choke, P., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Farerisa, P., Filzhugh, W., Gage, D., Galagan, J., Gardyas, S., Gord, S., Goyette, M., Graham, L., Gardyas, S., Gord, S., Goyette, M., Graham, L., Gardyas, S., Landers, T., Holme, W., Illev, I., Johnson, R., Jones, C., Kanata, A., Karatas, A., Kells, C., LaRocque, K., Landarses, R., Landers, T., Marche, M., Marthews, C., MacChand, P., McKernen, K., Marche, R., Liu, G., MacLean, C., MacGanald, P., Major, J., Levine, R., Matlen, S., Marche, M., Marche, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., O'Lver, J., Peterson, K., Phunkhang, P., Plerre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Roy, A., Santos, R., Schupback, R., Strauer, S., Schupback, R., Strauer, S., Schupback, R., Strauer, S., Schupback, R., Subramanian, A., Taalamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Marche, M., Travis, N., Trigildo, J., Vassiliev, H., Zanner, A. and Zody, M., Zannoun, J., Zembek, L., Zimmer, A. and Zody, M., Zannoun, J., Zembek, L., Zimmer, A. and Zody, M., Zannoun, J., Zembek, L., Zimmer, A. and Zody, M., Zannoun, J., Royer, S., Schupback, M., Stander, M., Statier, M., Marcher, M., Statier, M., Marcher, M., Walley, M., Marcher, M., Marcher, M., Marcher, M., Walley, M., Marcher, M., Marcher, M., Walley, M., Walley, M., M., Marcher, M., Walley, M., Walle
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Homo sapiens chromosome 8 clone RP11-1077M7 map 8, LOW-PASS SOCIENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (29-NOV-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                         Gaps
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1 (bases 1 to 64620)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
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* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
Length 31938;
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85.0%; Score 17; DB 2; Length 319
100.0%; Pred. No. 2e+03;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens chromosome 8, clone RP11-1077M7
Unpublished
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Center clone name: 1077_M_7
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HTG; HTGS_PHASE0.
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                                                                                                              17; Conservative
                                                                 Sest Local Similarity
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overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will 0747: gap of 100 bp 11391: contig of 644 bp in length 11391: contig of 648 bp in length 12174: contig of 683 bp in length 12967: contig of 683 bp in length 3067: gap of 100 bp 3067: gap of 100 bp 13749: contig of 682 bp in length 13749: contig of 682 bp in length 1849: gap of 100 bp 11 length 1458: contig of 709 bp in length 15347: contig of 689 bp in length 16153: contig of 689 bp in length 16153: contig of 689 bp in length 1633: gap of 100 bp 100 bp 1740: contig of 695 bp in length 1740: contig of 692 bp in length 18523: contig of 683 bp in length 18523: contig of 683 bp in length 18523: contig of 683 bp in length 19286: contig of 663 bp in length 19286: contig of 663 bp in length 775: gap of 100 bp 1433: contig of 658 bp in length 1533: gap of 100 bp of 100 bp contig of 705 bp in length of 100 bp contig of 678 bp in length 100 bp of 656 bp in length 100 bp of 662 bp in length 100 bp f 636 bp in length 100 bp . if 668 bp in length 100 bp ' f 689 bp in length :: gap of 100 bp 9179: contig of 677 bp in length b: gap of 100 bp 9942: contig of 663 bp in length 675: contig of 675 bp in length 100 bp . if 699 bp in length 100 bp of 676 bp in length 86: gap of 100 bp 20058: contig of 672 bp in length 20818: gap of 100 bp 2081: contig of 663 bp in length 121: gap of 100 bp 100 bp 2011: gap of 100 bp 2011: gap 2011: gap of 100 bp 2011: gap of 100 bp 2011: gap of 100 bp 2011 oof 100 bp contig of 605 bp in length 23: gap of 100 bp 23226: contig of 703 bp in length 26: gap of 100 bp 24014: contig of 688 bp in length 24015 24114: gap of 100 bp 24115 24806: contig of 692 bp in length 24807 24906: gap of 100 bp 25598: contig of 692 bp in length 25599 25598: contig of 682 bp in length 25699 26385: contig of 687 bp in length 26386 26485: gap of 100 bp 19: gap of 100 bp 22423: contig of 704 bp in length contig of contig of contig of contig of contig of 8502: gap of 10 9179: contig of contig of 8402: contig of 10647: com. 13749: cont 10747: gap of 11391: con 14658: gap of 15347: cont 3016: con 15447: gap of 22523: gap of 3872: gap of 4508: co. 8: gap of 5270: cor ): gap of 6038: cor gap of 7713: gap of 9279: gap of 3116: gap of 3772: cc 6138: gap c 6837: c 6837: c 6837: c 6837: c 6937: gap c 7613: c 2238: 11491: 17048: 12274: 2338: 13849: 17840: 18623: 20921: 21719: 23326: 4608: 10042: 19386: 5370: 13067 16253 20158 be preserved. 6603 8503 9180 1492

85.0%; Score 17; DB 2; Length 64620; 100.0%; Pred. No. 1.6e+03; ive 0; Mismatches 0; Indels ( 49445 49845 gap of 100 bp 1 ength 49845 50534 contig of 690 bp in length 50535 50634; gap of 100 bp 20535 50635 51322 contig of 698 bp in length 5133 51432; gap of 100 bp 52112 52211; gap of 100 bp 52112 52211; gap of 100 bp 52312 52312; gap of 100 bp 52973 52972; gap of 100 bp 52973 53605; contin of 61 bp in length 52973 28037 28720 28819: gap c. 288720 29475: contig of co. ... 29476 29575: gap of 100 bp -74 30265: contig of 690 bp in length -75 30265: contig of 690 bp in length -76 699 bp in length 198: gap of 100 bp 3656; contig of 668 bp in length 3755; gap of 100 bp 135; contig of 669 bp in length 135; gap of 100 bp 135; gap of 649 bp in length 136; gap of 649 bp in length 27145: contig of 660 bp in length 64: gap of 100 bp 1862: contig of 698 bp in length 62: gap of 100 bp 32676: contig of 714 bp in length 76: gap of 100 bp 33451: contig of 675 bp in length 34344: gap of 100 bp 35035: contig of 691 bp in length 35135: gap of 100 bp 35: gap of 100 bp 35798: contig of 663 bp in length 38184: gap of 100 bp 38877: contig of 693 bp in length 39977: gap of 100 bp 39675: contig of 698 bp in length 39775: gap of 100 bp 10429 40528: gap of 100 bp 1259 441202: contig of 674 bp in length 11203 41302: gap of 100 bp 11303 41991: contig of 689 bp in length 3519 43618: gap of 100 bp 3519 44309: contig of 691 bp in length 4410 44409: gap of 100 bp 4410 45082: contig of 680 bp in length 5083 45182: gap of 100 bp 55183 45862: contig of 680 bp in length 45962: gap of 100 bp 46613: contig of 651 bp in length 46713: gap of 100 bp 47378: contig of 665 bp in length .6714 47378: contry or co. 1.10 bp 17379 47478: gap of 100 bp 17479 48175: contig of 697 bp in length in length 775: gap of 100 bp 40428: contig of 653 bp in length 42860: gap of 100 bp 43518: contig of 658 bp in length p of 100 bp contig of 660 bp in length 18936 49035: gap of 100 bp 19036 49744: contig of 709 bp in length 52972: gap of 100 bp 53605: contig of 633 bp in length 27245: gap of 100 bp 27936: contig of 691 bp 27937 28036: gap of 100 bp 28037 28719: contig of 683 bp 51: gap of 100 bp 34244: contig of 693 bp gap of 100 bp 60: contig of 669 bp 33452 33551; gap of 40528: gap of 41202: cont 18176 48275: gap of 48276 48935: cont 42760: Query Match 85.0° Best Local Similarity 100.0 Matches 17; Conservative 31065 31164: 31165 318 31863 31962: 32677 32776: 35898: 36666: 37435: 42091: 35036 35135 6614 46713 10529 35799 9676 1992 34345

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Submitted (05-Nov-1998) Norimichi Nomura, Kyoto University, Lab. of
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/db_xref="taxon:306"
1766 c 1807 g 941 t
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                     /bound_moiety="NAD"
569 c 687 g
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Bacteria; Proteobacteria.
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2 (bases 1 to 6220)
/gene="enr"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (08-JAN-1998) F. Rohdich, TU Muenchen, Institut fuer Organische Chemie and Biochemie, Lichtenbergstr. 4, D- 85748
                                                                                                                                                                                                                                                                                                                                                                                                               Thermoanaerobacter group; Moorella group; Moorella.

(bases 1 to 2142)

Rohdich,F., Wiese,A., Feicht,R., Simon,H. and Bacher,A.

Enoate Reductases of Clostridia. CLONING, SEQUENCING, AND
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On Aug 7, 1998 this sequence version replaced gi:2791351.
Related sequence: Y09960.
Location/Qualifiers
                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                       Moorella thermoacetica
Bacteria; Firmicutes; Bacillus/Clostridium group;
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/strain="DSM 1974"
/db_xref="taxon:1525"
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/protein_id="CAA76082.1"
/db_xref="G1:3402836"
/db_xref="SPTREMBL:052935"
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1590. .1626
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/gene="enr"
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32. .2050
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3 (bases 1 to 2142)
Rohdich, F.
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                                  X16136.1 GI:3402835
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AB019552 6220 bp DNA linear BCT 18-JAN-2002 Aeropyrum pernix genes for 16S rRNA, ITS, 23S rRNA, partial and complete sequence, strain:OH2.
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Datent: WO 0107589-A 5 01-FEB-2001;
THE INSTITUTE FOR GENOMIC RESEARCH (US); QIAGEN GmbH (DE);
Gesellschaft fuer Blotechnologische Forschung mbH (GBF) (DE);
Deutsches Krebsforschungszentrum Stiftung des Oeffentliche Rechts
(DE); Medizinische Hochschule Hannover (DE)
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                                                                                                                                                                                                                                                                                                                                                                                       linear PAT 22-FEB-2001
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Aeropyrum pernix
Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
Desulfurococcaceae; Aeropyrum.
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84.0%; Score 16.8; DB 1; Length 2142; 90.0%; Pred. No. 5.7e+03; tive 0; Mismatches 2; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (16-JAN-2002) Norimichi Nomura, Kyoto University,
Division of Applied Biosciences, Graduate School of Agriculture,
Sakyo, Kyoto 606-8502, Japan
(E-mail:j54718@sakura.kudpc.kyoto-u.ac.jp, Tel:81-75-753-6224,
Marine Microbiology, Graduate School of Agriculture;
Kitashirakawa-Oiwake-cho, Sakyo-ku, Kyoto 606-8502, Japan
(E-mail:1547188aakura.kudpc.Kyoto-u.ac.jp, Tel:81-75-753-6219,
Fax:81-75-753-6226,
On Jan 18, 2002 this sequence version replaced gi:3869179.
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AB078015
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1799. .2155
/note="internal transcribed spacer (ITS) region"
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/note="internal transcribed spacer (ITS) region"
2156. .5238
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298. 1797
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/product="23S ribosomal
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298. .1797
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6220 bp DNA linear BCT 19-JAN-2002 Aeropyrum pernix genes for 16s rRNA, 23s rRNA and ITs region, complete sequence, strain:OH3.
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Nomura, N.
Nomura, N.
Direct Submission
Submitted (16-JAN-2002) Norimichi Nomura, Kyoto University,
Division of Applied Biosciences, Graduate School of Agriculture;
Sakyo, Kyoto 606-8502, Japan
(E-mail:j54718@sakura.kudpc.kyoto-u.ac.jp, Tel:81-75-753-6224,
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/note="internal transcribed spacer (ITS) region"
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/gene="arnL"
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Desulfurococcaceae; Aeropyrum.
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/organism="Aeropyrum pernix"
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Micromonospora meg Mycobacterium tube Porcine muscular s

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June 19, 2002, 16:50:44 ; Search time 3798.65 Seconds (Without alignments) 9.040 Million cell updates/sec
  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                       1736436 seqs, 858457221 residues
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/net/abss06/SIDS1/gcgdata/hold-geneseq/geneseqn-embl/NA2002.DAT:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Human cervical can Mycobacterium tube Human sbg34976IGBa PAM polynucleotide PAM encoding cDNA. Encodes Rat C-term Pseudomonas sp lip CFDV-DNA fragment CFDV-DNA fragment Description SUMMARIES AAF26319 AAH68825 AA166138 AAQ11038 AAX02689 AAH52030 AA166145 AAD16357 ΩI 2222220 2222220 12222220 Match Length DB 2238 2388 3217 3226 100.0 100.0 84.0 80.0 79.0 79.0 79.0 79.0 Query 20 20 16.8 15.8 15.8 15.8 15.8 Score Result 26450786 Š. 0000

	DNA encoding novel Drosophila melanog Trans-feruloy1 SCO HSV-2 strain SB5 C Streptococcus olea HSV-2 strain SB5 C Human herpesvirus DNA methyltransfer Human immune/haema	t region.  irus; CFDV; bacterial promoter; phloem-specific; CaMV 35S promoter; ss.  rs  nds to nucleotides 16 to 22"  nds to nucleotides 4 to 10"	to nucleotides 38 to 43"
AAQ05637 AAS10277 AAS59517 AAL36348 AAR39682176 AAS62176 AAR3926 AAS62178 AAR93201 AAK93201 AAK93300	AASB680 ABL09000 ABL09000 AAV62156 AAV62176 AAV6912 AAV8912 AAK81520 AAK81520 AAK81520 AAK81520 AAK81520 AAK81520 AAK81520 AAK81520 AAK81520	Alphea $C_i$ ,	e Region binds
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                                                                                                                                                                                                               This invention describes a coconut foliar decay virus (CFDV) DNA fragment that includes the stem-loop structure of CFDV DNA but lacks the translation start codons of open reading frames ORF1 and/Or ORF2. The new CFDV DNA fragment is useful as a bacterial or yeast promoter, as a promoter for tissue-specific (especially phloem-specific) gene expression in plants and for production of chimeric constructs for transient or stable expression. Certain fragments of CFDV DNA have stronger promoter
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/note= "Region binds to nucleotides 27 to 32"
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                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
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This invention describes a coconut foliar decay virus (CFDV) DNA fragment that includes the stem-loop structure of CFDV DNA but lacks the translation start codons of open reading frames ORF1 and/or ORF2. The new CFDV DNA fragment is useful as a bacterial or yeast promoter, as a promoter for tissue-specific (especially phloem-specific) gene expression in plants and for production of chimeric constructs for transient or stable expression. Certain fragments of CFDV DNA have stronger promoter activity in E. coli than the CaMV 35s promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lipopeptide synthase; transgenic plant; antiviral; antibacterial; antifungal; surfactant; microbial depollution; emulsifier; tertiary crude oil recovery; ORF08563; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coconut foliar decay virus promoters - for gene expression in
                                                                                                       /note= "Region binds to nucleotides 27 to 32"
"Region binds to nucleotides 38 to 43"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 20; DB 20; Length 44; 100.0%; Pred. No. 6.3; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Becker D, Hehn A, Randles JW, Rohde W, Salamini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas sp lipopeptide synthase DNA ORF08563.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 44 BP; 8 A; 16 C; 17 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TIGR-) TIGR INST GENOMIC RES.
(QIEG) GES BIOTECHNOLOGISCHE FORSCHUNG MBH.
(BDKF2-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 4; 12pp; German.
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(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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             QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δλ
                                                                                                                                                                                                                                           This invention describes a novel DNA sequence (I) that expresses products having the biological function of lipopeptide synthase. The invention also describes (I) recombinant expression vectors containing (I); (2) production and eukaryotic cells transformed or transfected with (I) or the vector of (2); (4) expression products (II) of (I), and synthetic proteins or peptides with the same sequences; (5) mono- or poly-clonal antibodies or peptides with the same sequences; (5) mono- or poly-clonal antibodies (Ab) specific for (II); (6) hybridoma cells that produce monoclonal Ab; and their crayments, are useful for expression of recombinant lipopeptide synthases, and as probes and primers for detection, isolation and milification of full-length cDNA sequences. (I) are used to produce transgenic plants. Lipopeptide synthases are useful for production of transgenic plants. Lipopeptide synthases are useful for production of antiviral, antibacterial or antifungal lipopeptides, particularly useful contains and or production of inopeptides synthases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;;
0
                                                                                                                                           producing antimicrobial agents, surfactants with increased bloavailability in microbial depollution methods, and transgenic plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used for increasing bioavailability in microbial depollution processes (acting as emulsifiers) and in tertiary crude oil recovery. Individual subunits from different lipopeptide synthases may be combined to allow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                        New DNA encoding a bacterial lipopeptide synthase, useful e.g. for
                                           Hilbert H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.0%; Score 16.8; DB 22; Length 5451; 90.0%; Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               synthesis of many different biologically active substances.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5451 BP; 937 A; 1766 C; 1807 G; 941 T; 0 other;
                                       Duesterhoeft A,
n S, Golyshin P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 16.0, ___Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cervical cancer marker nucleic acid 99.
                                 Tuemmler B, Hoheisel J, Duest
Moore E, Straetz M, Heim S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
 (MEDI-) MEDIZINISCHE HOCHSCHULE HANNOVER.
                                                                                                                                                                                                             Claim 3a; Page 28-30; 33pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAH68825 standard; cDNA; 341 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0171350.
2000US-0189315.
2000US-0203791.
2000US-0210600.
2000US-022104.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ctacccggccgaaggccggg 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 90.0
nes 18; Conservative
                                                                                      WPI; 2001-159715/16.
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09-JUN-2000;
21-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-DEC-1999;
                                     Fraser CM,
                                                    Timmis KN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH68825;
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This invention relates to a method for identifying a nucleotide or polypeptide sequence that may be a drug target, or essential for growth or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092
                                                                                                                                                                                                  cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be
                                                                                                                                                                              The invention relates to novel genes (AAH68727-AAH73383) associated with
                                                                            New isolated nucleic acid for diagnosing and treating cervical cancer and for assessing and detecting compounds for treating the cancer - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying nucleotide or polypeptide sequence for use as drug target, involves providing algorithm that analyzes a functional relationship between nucleotide or polypeptide sequences, and comparing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis potential drug target gene SEQ ID 84.
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                                                                                                                                                                                                                                                                                                                                                                                                                             80.0%; Score 16; DB 22; Length 341; 94.1%; Pred. No. 3.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                             Sequence 341 BP; 72 A; 93 C; 93 G; 68 T; 15 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 3.2e+02;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
Schlegel R, Deeds J, Berger A, Zhao X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 103-104; 207pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Marcotte EM;
                                                                                                                                    Claim 1; Page 120; 1051pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH52030 standard; DNA; 2040 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0165124.
2000US-0179531.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0165086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eisenberg D, Rotstein SH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 cenggecgaaggeeggg 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 cccggccgaaggccggg 20
                                                                                                                                                                                                                                                                                                                       useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (REGC ) UNIV CALIFORNIA
                                      WPI; 2001-375006/39.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAG81179.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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represent DNA encoding proteins AAGB1096 - AAGB1241, Mycobacterium tuberculosis proteins which are potential drug targets. The DNA and protein sequences are used to illustrate the method of the invention. The method involves providing an unknown nucleotide or polypeptide sequences, and comparing it to a number of sequences along with at least one algorithm capable of analysing a functional relationship between nucleotide and polypeptide sequences. The method is useful for characterising the innotion of nucleic acids and polypeptides that may be useful as a target for a drug or essential for the growth or viability of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New secreted and membrane associated polypeptides for treating Alzheimer's disease, psoriasis, cancer, enterocolitis, sleep and sexual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; Alzheimer's disease; amyotrophic lateral sclerosis; ALS; Zollinger-Ellison syndrome; immune system disease; schizophrenia; inflammation; haematopoietic disease; anxiety; feeding disorder; aging; anorexia; depression; cardiovascular disease; sleep disorder; seizure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           memory alteration; migraine; stroke; asthma; neuropathy; hypoglycaemia; sexual disorder; growth abnormality; infection; autoimmune disease; rheumatoid arthritis; cataractogenesis; angiogenesis; atherosclerosis; cerebral ischemaia; cirrhosis; Huntington's disease; Hodgson's disease; hypercholesterolaemia; headache; amnesia; cardiac arrhythmia; obesity; diabetes mellitus; glomerulonephritis; renovascular hypertension; cancer; vaccine; gene therapy; sbg34976IGBa gene; ds.
                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                           Length 2040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith RF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= a
/product= "Human sbg34976IGBa protein #1"
                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                   Sequence 2040 BP; 374 A; 673 C; 671 G; 322 T; 0 other;
                                                                                                                                                                                                                                                                         79.0%; Score 15.8; DB 22;
89.5%; Pred. No. 3.5e+02;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Agarwal P, Kabnick KS, Murdoch PR, Rizvi SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SMIK ) SMITHKLINE BEECHAM CORP. (SMIK ) SMITHKLINE BEECHAM PLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAD16357 standard; DNA; 2238 BP.
                                                                                                                                                                                                                                                                                                                                                                                             1731 taccqqqccgacgqccggg 1749
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2000US-0198583.
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                                                                                                                                                                                                                                                                                                                                                         2 tacccggccgaaggccggg 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human sbq34976IGBa gene #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 89.5'
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .2238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-FEB-2000;
18-APR-2000;
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                                                                                                                                                                                     an organism
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
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           555555555555<del>×</del>8
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The present sequence is a gene encoding numan suggraphores.

The present sequence is a gene encoding such polypeptides.

The invention relates to secreted and membrane associated polypeptides

The invention relates to secreted and membrane associated polypeptides

The invention are useful for treating diseases such as Alzheimer's disease,

and nucleic acid molecules encoding such polypeptides. Sequences of the

convertion are useful for treating diseases such as Alzheimer's disease,

amyotrophic lateral sclerosis (ALS), Zollinger-Ellison syndrome, diseases,

cof the immune system, heematopoletic disease, inflammation, anxiety,

schizophrenia, feeding disorders, anorexia, depression, social, sexual

con rewarded behaviour, cardiovascular disease, sleep disorder, learning

and memory alteration and altered immune response, setzure, migraine,

cancer, stroke, asthma, neuropathy, aging, sexual disorders, treatment

cof transsexuals, growth abnormalities, obesity, infections, autoimmune

cof transsexuals, growth abnormalities, obesity, infections, autoimmune

cof diseases (e.g. rheumatoid arthritis), cataractogenesis, angiogenesis,

diseases (e.g. rheumatoid arthritis), cataractogenesis, angiogenesis,

clischaemia, atherosclerosis, cirrhosis, Huntington's disease, headache,

crepair of acute and chronic mucosal lesion, lung carcinoma, cerebral

congestive heart failure, cardiac arrhythmias, hypercholesterolaemia,

congestive heart failure, cardiac arrhythmias
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amidase gene and modifying application of its expressed active products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                 The present sequence is a gene encoding human sbg34976IGBa protein,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 2238;
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Pred. No. 3.4e+02;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SHAN-) SHANGHAI BIO-CHEM INST CHINESE ACAD SCI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptidylglycine alpha-amidating monooxygenase.
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                                             Claim 2; Page 48-49; 94pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAI66145 standard; cDNA; 2388 BP.
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disorders, stroke, and asthma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79.0%;
89.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97CN-0106382.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 tacccggccgaaggccggg 20
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les 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression studies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-DEC-1997.
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obtain three rPAM gene fragments, then through technologies of point mutation and PCR recombination to splice rPAM holoenzyme gene and form its eucaryon expression plasmid so as to obtain the active expression in CHO cell. The obtained expression product can be directly used for amidation modification of polypeptide and protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-0CT-1989;
26-MAR-1990;
                                                                                                                                                                                                                                                                                                      17-MAY-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 - APR - 1990;
                                                                                                                                                                                                                                                                             AAQ11038;
                                                                                                                                                                                                                                        AAQ11038/C
                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                         qq
      22222X
                                                                                                                                                                                                                                                                                         δ
                                             The invention relates to a rat amidase gene, peptidylglycine alpha-amidating monooxygenase/PAM (EC1.14.17.3) and its active expression product in Chinese hamster ovary (CHO) cell. The invention uses in situ hybridization and a polymerase redin reaction (PCR) method to screen and obtain three rPAM gene fragments, then through technologies of point mutation and PCR recombination to splice rPAM holoenzyme gene and form its eucaryon expression plasmid so as to obtain the active expression in CHO cell. The obtained expression product can be directly used for amidation modification of polypeptide and protein. The present sequence is that of a polynucleotide of the PAM gene (AAI66138), useful to the
                                                                                                                                                                                                                                                               ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a rat amidase gene, peptidylglycine alpha-amidating monooxygenase/PAM (EC1.14.17.3) and its active expression product in Chinese hamster ovary (CHO) cell. The invention uses in situ hybridization and a polymerase chain reaction (PCR) method to screen and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Amidase gene and modifying application of its expressed active products
                                                                                                                                                                                                                                                                 Gaps
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0
                                                                                                                                                                                                                                  79.0%; Score 15.8; DB 22; Length 2388; 89.5%; Pred. No. 3.4e+02; ive 0; Mismatches 2; Indels 0;
                                                                                                                                                                                               Sequence 2388 BP; 638 A; 549 C; 589 G; 612 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptidylglycine alpha-amidating monooxygenase; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "PAM"
/EC_number= "1.14.17.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                       Example 1; Fig 2; 37pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                     AAI66138 standard; cDNA; 3217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Fig 1; 37pp; Chinese.
                                                                                                                                                                                                                                                                                                          1823 CTACCCGGGCGAAGGCTGG 1805
                                                                                                                                                                                                                                                                                     1 ctacccggccgaaggccgg 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chinese hamster ovary; PAM;
                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                         Query Match
Best Local Similarity 89.55
  to polypeptide amidating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to polypeptide amidating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .2629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jiang Z, Xia Q;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-590349/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                              PAM encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAM51684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                    14-JAN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-APR-1997;
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                                                                                                                                                                       invention
                                                                                                                                                                                                                                                                                                                                                                                              AA166138;
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                                                                                                                                                                                                                                                                                                                                                           AAI66138/c
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qq
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New enzymes useful in peptide C-amidation - convert peptide C-terminal glycine to alpha hydroxy glycine then remove this leaving
                                                                                                                                    .
0
                                                                                 Length 3217;
                                                                                                                              Indels
Sequence 3217 BP; 839 A; 762 C; 791 G; 825 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3226 BP; 845 A; 748 C; 788 G; 844 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C-terminal amidating enzyme; calcitonin; gastrin; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= C-terminal amidating enzyme
                                                                         79.0%; Score 15.8; DB 22;
89.5%; Pred. No. 3.4e+02;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Encodes Rat C-terminal amidating enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 6; 114pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amidating enzyme from the horse.
See also AAQ11039-Q11042.
                                                                                                                                                                                                                                                                                                                                                    AAQ11038 standard; cDNA; 3226
                                                                                                                                                                                                        2652 CTACCCGGCCAAGCTGG 2634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89JP-0281933.
90JP-0076331.
90JP-0106412.
90JP-0205475.
                                                                                                                                                                           1 ctacccggccgaaggccgg 19
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                                                       Query Match ,...
Best Local Similarity 89.59
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            terminal glycine to a peptide C-term amide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1991-087274/12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAR11110
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79.0%; Score 15.8; DB 12; Length 3226; 89.5%; Pred. No. 3.3e+02;

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Amidation; post-translational modification; AE; ss.
                                                                    Rattus rattus.
                                                                                                                                                                                                                                                                                                                             01-FEB-1990;
                                                                                                                                                                                                                                     AU9049043-A.
                                                                                                                                                                                                                                                                                 29-NOV-1990.
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                                                                                                                  Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence hybridises, under stringent conditions, with a DNA sequence (I) which encodes an alpha amidating enzyme (AEE) and is foreign to the host cell into which it is transformed. (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vector. The AEE encoded is used as a catalyst in the conversion of a peptidyl substrate to a corresp. peptidyl amide. This can be used for making a protein biologically active, e.g. calcitonin or growth hormone releasing factor. See also AAQ05638.
                                                                                                                                                                                                                                                                                                                                                        Sequence which hybrdises with DNA encoding alpha amidating enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is connected to a promoter and is contained in an expression vector. The AEE encoded is used as a catalyst in the conversion
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       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prodn. of alpha amidating enzyme – using prokaryotic or eukaryotic expression vectors having transcriptional promoter
       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                      Alpha amidating enzyme; peptidyl amide; ss.
       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Beaudry GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers 346..2907
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                                                                                                                                                                                                     637/c
AAQ05637 standard; DNA; 3586 BP
       0;
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                                                                                2585 CTACCCGGCCGAAGGCTGG 2567
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                                                     1 ctacccggccgaaggccgg 19
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                                                                                                                                                                                                                                                                                                              14-DEC-1990 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag= a
       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Betelsen AH, Mehta NM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UNIG-) UNIGENE LAB INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1990-248308/33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-FEB-1989;
       17;
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                                                                                                                                                                                                                                                                  AAQ05637;
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                                                                                                                                                                          RESULT 10
            Matches
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                                                                                                                                                                                                AAQ05637,
                                                                                                                                                                                                                                                                                                                                       E STANDER STAN
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Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The DNA was isolated from libraries prepd. from RNA extracted from rat medullary thyroid carcinoma tissues or derived cell lines such as IVI 10028. The CDNAs extracted could be divided into distinct types, the sequence below being of Type A. (Type B is given in AAQ10278). The sequence can be inserted into expression vectors for the prodn. of recombinant alpha-amidating anzyme (AE) useful for post translational modification of other recombinant polypeptides such as calcitonin. The sequence includes a membrane spanning comain which may be undesirable in a recombinant DNA expression system, possibly inactivating the enzyme. A stop codon can be placed upstream of the domain-encoding sequence, pref. between placed upstream of the domain-encoding sequence. This results in the consession of a 75 rather than 94 kD. The sequence of Type A and Type B are substantially identical with the exception of an intron region from bases 1178-1492 (CDS) of the Type B CDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expression systems for amidating enzyme - comprises prokaryotic or euraryotic hosts contg. a recombinant expression vector contg. the corresp. DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Pred. No. 3.3e+02;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3586 BP; 909 A; 879 C; 906 G; 892 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Betelsen AH, Mehta NM, Beaudry GA;
Location/Qualifiers 346..2907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 2; 52pp; English.
                                                                                                                 /label= AE Type A
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89.5%;
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Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UNIG-) UNIGENE LAB INC.
                                                                                      /*tag=
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P-PSDB; AAR10322.
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Sequence 4185 BP; 713 A; 1363 C; 1307 G; 802 T; 0 other;

XX SO

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(GETH ) GENENTECH INC.
                                                                                                                                      WPI; 2001-408281/43.
                                                                                                                                          P-PSDB; AAU12205.
         WO200140466-A2.
   Homo sapiens
                                                                    18-FEB-2000;
18-FEB-2000;
                                                                           22-FEB-2000;
                                                                              24-FEB-2000;
                                                                                 24-FEB-2000;
                                                                                        20-MAR-2000;
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                                                                                           21-MAR-2000;
                                                     20-DEC-1999;
                                                           06-JAN-2000;
               07-JUN-2001
                                  02-DEC-1999
                                            09-DEC-1999;
                                        02-DEC-3
                                     02-DEC-
                                                  20-DEC-
                                                                                                                                                         lung,
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AAS21244-AAS21518 encode for novel human secretory and transmembrane
PRO polypeptides. The PRO polypeptides are useful to detect other
PRO polypeptides, to link bloactive molecules to cells expressing
PRO polypeptides, to modulate biological activities of cells expressing
PRO polypeptides, and to detect the presence of mammalian lung, colon,
Dreast, prostate, rectal, cervical or liver tumours by comparing PRO
Dreast, prostate, rectal, cervical or liver tumours by comparing PRO
Some of the 275 sequences are also useful to stimulate the release of
tumour necrosis factor-alpha (TNF-alpha) from human blood, the
proliferation or differentiation of chondrocytes, the proliferation or
gene expression in pericyte cells, the release of proteoglycans from
cartilage, the proliferation of inner ear utricular supporting cells or
for 1-lymphocytes, the release of a cytokine from peripheral blood
monocytes (PBMCs), or the proliferation of endothelial cells. Some of
the PRO polypeptides may modulate glucose or free fatty acid uptake by
skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
co factor VIIA. The PRO polypeptides can be used in assays to identify
molecules involved in binding interactions. The polynuclectides encoding
PRO polypeptides can be used to generate probes, antisense RNA/DNA,
transgenic or knock out animals and can be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gao W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Deforge L, Desnoyers L, Filvaroff E, G;
A, Godowski PJ, Gurney AL, Sherwood S;
Tumas D, Watanabe CK, Wood WI, Zhang Z;
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01-DEC-2000; 2000WO-US32678
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2000WO-US08439.
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Gerritsen ME, Goddard A,
Smith V, Stewart TA, Tum
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Sequences AAS59506-AAS59804 represent DNA molecules encoding
Propionibacterium acnes immunogenic polypeptides. The proteins and their
Propionibacterium acnes immunogenic polypeptides. The proteins and the cassociated DNA sequences are used in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and costeomyellitis), uveitis and endophthalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in a patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and cused to downregulate expression and activity of P. acnes polypeptides and diagnostic agents for determining P. acnes presence, for example, by cance linked immunosorbent assay (ELISA). This sequence encodes the polypeptides shown in AAU42344-44248 and AAU67479.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                                                                                                                                                                                                                                        SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant; ds.
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for
                                                   0;
       Length 4185;
                                                                                                                                                                                                                                                                                                                                                                            Propionibacterium acnes immunogenic protein encoding DNA #12.
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L'maisonneuve J, Zhang Y, Jen S, Carter D;
                                                 Indels
  79.0%; Score 15.8; DB 22;
89.5%; Pred. No. 3.3e+02;
iive 0; Mismatches 2;
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                                                                                                                                                                                                                                           AAS59517 standard; DNA; 18796 BP.
                                                                                                                                1820 TACCCGGCCGCAGGCCGCG 1802
                                                                                        2 tacccggccgaaggccggg 20
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02-JUN-2000; 2000US-208841P.
07-JUL-2000; 2000US-216747P.
                                                                                                                                                                                                                                                                                                                                    (first entry)
                                          17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Propionibacterium acnes.
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                         Best Local Similarity
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Query Match
                                            Matches
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08-SEP-2000; 20000S-0231413.
08-SEP-2000; 20000S-0231413.
08-SEP-2000; 20000S-0231414.
08-SEP-2000; 20000S-0232080.
14-SEP-2000; 20000S-0232081.
14-SEP-2000; 20000S-023398.
14-SEP-2000; 20000S-0232398.
14-SEP-2000; 20000S-0232399.
14-SEP-2000; 20000S-0232399.
14-SEP-2000; 20000S-0232399.
14-SEP-2000; 20000S-0232401.
14-SEP-2000; 20000S-0232401.
14-SEP-2000; 20000S-0233063.
14-SEP-2000; 20000S-0233063.
14-SEP-2000; 20000S-0233063.
14-SEP-2000; 20000S-0233063.
14-SEP-2000; 20000S-0233063.
15-SEP-2000; 20000S-0234098.
25-SEP-2000; 20000S-02344998.
26-SEP-2000; 20000S-02344998.
27-SEP-2000; 20000S-0234484.
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2000US-024021.
2000US-024121.
2000US-0241785.
2000US-0241786.
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2000US-0237040.
2000US-0239935.
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2000US-0241826.
2000US-0244617.
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20000S-0246475.
20000S-0246475.
20000S-0246476.
20000S-0246477.
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2000US-0249208.
2000US-0249209.
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2000US-0230438.
2000US-0231242.
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2000US-0235836.
2000US-0236327.
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02-0CT-2000; 2000US-0237037.
02-0CT-2000; 2000US-0237038.
02-0CT-2000; 2000US-0237039.
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2000US-0236368
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                                                              2000US-0229344
                                                                                2000US-0229345
                                                                                               2000US-0229509
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20-OCT-2000; 2
20-OCT-2000; 2
01-NOV-2000; 2
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05-SEP-2000; 2
05-SEP-2000; 2
06-SEP-2000; 2
06-SEP-2000; 2
08-SEP-2000; 2
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29-SEP-2000;
29-SEP-2000;
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13-OCT-2000;
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20-OCT-2000;
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17-NOV-2000;
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                               01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
0
                                                                                                                                                                                                                                                                                                                                                                                                   Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antiingal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; musculoskeletal system; ds.
                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                    Human musculoskeletal system related polynucleotide SEQ ID NO 2713.
                                                                                                                  ;
                                                                                     Length 18796;
                                    Sequence 18796 BP; 3824 A; 5690 C; 5570 G; 3711 T; 1 other;
                                                                                                                      Indels
                                                                                     Score 15.4; DB 23;
Pred. No. 4.4e+02;
0; Mismatches 1;
     at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                          AAL36348 standard; DNA; 19820 BP
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2000US-0225266.
2000US-0225267.
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2000US-0226681.
2000US-0226868.
2000US-0227182.
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2000US-0190076.
2000US-0198123.
2000US-0205515.
2000US-0214886.
2000US-0214886.
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2000US-0218290.
2000US-0220963.
2000US-0220964.
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2000US-0224519.
2000US-0225213.
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2000US-0225270.
                                                                                     Query Match 77.0%;
Best Local Similarity 94.1%;
Matches 16; Conservative (
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2000US-0217487
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16-MAR-2000; 2000US-0189874
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                                                                                                                                                                                        9479 CCCGGACGAAGGCCGGG 9463
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26-JUL-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
14-JUL-2000;
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18-APR-2000;
19-MAY-2000;
07-JUN-2000;
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22-AUG-2000;
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          SXS
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CDS
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                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to novel genes (AAL34669-AAL37666) and proteins (ABB03087-ABB04109) associated with the musculoskeletal system useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human its sues disclosed in the specification. The nucleic acids, proteins, antibodies and (anti)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and cher cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune tract, liver, lung, or urogenital; (b) immune anemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple scierosis, rhemmatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as mycoradial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 parasitic infections.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; SEQ ID NO 2713; 781pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 19820 BP; 6182 A; 3722 C; 4043 G; 5871 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barash SC, Ruben SM;
                                                                                                                                                                                                                                     2000US-0249300.
2000US-0250160.
2000US-0250391.
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                                              2000US-0249213.
2000US-0249214.
                  2000US-0249211
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Gaps

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Score 15.4; DB 22; Length 19820; Pred. No. 4.4e+02; 0; Mismatches 1; Indels 0;

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Best Local Similarity 94.1%; Pred. No. 4.1e+02;
Matches 16; Conservative 0; Mismatches 1;
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June 19, 2002, 15:47:08; Search time 247.21 Seconds (without alignments) 19.872 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Gapop 10.0 , Gapext 1.0
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Listing first 45 summaries

Issued\_Patents\_NA:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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SUMMARIES	ID	US-09-462-975-7	US-09-462-975-1	US-08-070-301-10	US-09-103-840A-1	US-08-225-477B-1	PCT-US95-04353-1	US-09-428-517-1	US-08-866-340-31	US-09-103-875-37	US-08-457-797A-9	US-08-812-025-9	US-09-138-873A-9	US-08-841-483-3	US-09-382-911-3	US-08-841-483-5	US-09-382-911-5		-403-852D-1	US-08-510-646B-15	US-09-231-818-15	US-08-725-182C-1	US-09-013-150-1	US-09-359-503-1	US-09-062-422-1	US-09-396-184-1	US-08-937-263B-1	US-08-791-495-8
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	Score	20	20	15.8	15.4	15.2	15.2	15.2	14.8	14.8	٠	14.8	٠			14.8		14.8	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4
	Result No.	П	7	c 3	4	ഗ	9	7		ნ <u>;</u>	10	11	12	c 13			c 16	17	87	13	20	7.7	22	23	24	25	56	27

Patent No. 5212296 Sequence 2, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 69, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 16, Appl Sequence 31, Appl Sequence 32, Appl		Sequence:/note-synthetic	s
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28 14.4 72.0 14.2 71.0 14.2 71.0 14.2 71.0 14.2 71.0 14.2 71.0 14.2 71.0 14.2 71.0 14.2 71.0 14.2 71.0 14.2 71.0 14.2 71.0 14.2 71.0 14.2 71.0 14.2 71.0 14.2 71.0 14.2 71.0 14.2 71.0 14.2 14.3 8 69.0 14.2 13.8 69.0 14.3 13.8 69.0 14.4 13.8 69.0 14.5 13.5 14.5 14.5 14.5 14.5 14.5 14.5 14.5 14	ALIGNM  SESULT 1  1S-09-462-975-7  Sequence 7, Application US/09462975  Patent No. 6303345  GENERAL INFORMATION: APPLICANT: Rohde, Wolfgang APPLICANT: Randles, John W. APPLICANT: Randles, John W. APPLICANT: Backer, Dieter APPLICANT: Backer, Dieter APPLICANT: Backer, Dieter APPLICANT: Balmini, Francesco TITLE OF INVENTION: USE OF VIRUS DNA AS FILE REPRENCE: 22232.000311 CURRENT APPLICATION NUMBER: US/09/462,97 CURRENT FILING DATE: 2000-05-17	PRIOR APPLICATION NUMB PRIOR FILING DATE: 19 PRIOR PELICATION NUMB PRIOR FILING DATE: 19 NUMBER OF SEQ ID NOS: SEQ ID NO 7 LENGTH: 21 TYPE: DNA ORGANISM: Artificial FEATURE: COTHER INFORMATION: CO OTHER INFORMATION: CO	i. Local Similarity hes 20; Conserva 1 ctacccggccgaagg
0 0 0 0 00000	RESULT Seque Pate Rate APPP APPP APPP TITI CURI	PRR SCO	Best Matc Oy Oy Db Db Seque Seque Gene APP APP APP APP APP APP APP

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APPLICANT: KISHIMOTO, JIRO
APPLICANT: KISHIMOTO, JIRO
APPLICANT: KAFO, TCHIKO
APPLICANT: KAFO, TCHIKO
TITLE OF INVENTION: ENZYME PARTICIPATING IN C-TERMINAL
TITLE OF INVENTION: AMIDATION, AND METHOD OF PREPARING SAME AND USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence:/note=synthetic OTHER INFORMATION: construct
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Best Local Similarity 100.0%; Score 20; DB 4; Length 1291;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
SORTREMT APPLICATION DATA:
APPLICATION NUMBER: US/08/070,301
FILING DATE: 24-MAY-1991
PRIOR APPLICATION: 435
                            CURRENT APPLICATION NUMBER: US/09/462,975
CURRENT FILING DATE: 2000-05-17
PRIOR APPLICATION NUMBER: PCT/EP98/04345
PRIOR FILING DATE: 1998-07-13
PRIOR FILING DATE: 1997-07-16
SUMBER OF SEG ID NOS: 7
SOFTWARE: FASTSEQ FOR Windows Version 4.0
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24-APR-1990
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APPLICATION NUMBER: JP 1-209687
FILING DATE: 15-AUG-1989
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APPLICATION MINITALY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/08070301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: IIDA, Toshio
APPLICANT: KAMINUMA, Toshihiko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 1072 ctacceggccgaaggccggg 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: FUSE, Yuka APPLICANT: TAJIMA, Masahiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ctacccggccgaaggccggg 20
                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
           23232.0003U1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
ZIP: 20036-8218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-070-301-10/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                             SEQ ID NO 1
LENGTH: 1291
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                                                                                                                                                                                                                                                                                                                                                                     US-09-462-975-1
                                                                                                                                                                                                                                                            TYPE: DNA
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APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VERSER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FITHE REFERENCE: 24366-22007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77.0%; Score 15.4; DB 4; Length 4411529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 3226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 34;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 64;
APPLICATION NUMBER: JP 2-205475
FILING DATE: 02-ANG-1990
ATTORNEY, FAGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: P-450-22830
TELECOMMUNICATION INFORMATION:
TELECHONE: (202) 887-040
TELEFAX: (202) 835-0605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79.0%; Score 15.8;
89.5%; Pred. No. 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 1, Application US/08225477B; Patent No. 5635370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09103840A patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.08; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, RODert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 440706
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 3226 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ctacccggccgaaggccgg 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 89.59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 77.0
Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                           single
                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: singl
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                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CORIGINAL SOURCE: ORGANISM: Rat
                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 4411529
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US-08-225-477B-1
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Betlach, Mary C.
APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: Shah, Sanjay Krishnakant
APPLICANT: McDaniel, Robert
APPLICANT: Tang, Li
TILLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE SYNTHASE
FILLE REPERENCE: 30062-20029,00
CURRENT APPLICATION NUMBER: US/09/428,517
CURRENT FILING DATE: 1999-10-28
EARLIER FILING DATE: 1999-10-28
EARLIER FILING DATE: 1999-10-26
EARLIER FILING DATE: 1998-10-29
NUMBER OF SEC ID NOS: 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.0%; Score 15.2; DB 4; Length 50937; 85.0%; Pred. No. 92; tive 0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                             1751-P0004
                                                                                                                                                                                                                                                                                                                                                                                                                            DESCRIPTION: DNA encoding a protein
                        APPLICATION NUMBER: PCT/US95/04353
                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/225,477
FILING DATE: April 8, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                     REGISTRATION NUMBER: 32423
REGISTRATION NUMBER: 1751-
TELECOMMULICATION INFORMATION:
TELEPHONE: 203-324-6155
TRIEFPAX: 203-327-1096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09428517
Patent No. 6251636
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE: entire sequence
IMMEDIATE SOURCE: rat brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 34916 cttcctggccgaaggccgcg 34935
                                                                                                                                                                                                                                                     TELEFAX: 203-327-1096
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50 CCACGCGCCAAAGGCCGGG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ctacccggccgaaggccggg 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ctacccggccgaaggccggg 20
                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGIH: 1520 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 85.0
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: rat BEHAB PCT-US95-04353-1
                                                                                                                                                                                                                                                                                                                                                                                      linear
                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                FRAGMENT TYPE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCETTER...
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-428-517-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-428-517-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 76.0%; Score 15.2; DB 1; Length 1520; Best Local Similarity 85.0%; Pred. No. 1.2e+02; Matches 17; Conservative 0; Mismatches 3; Indels 0;
                                                                                                                              E: St. Onge Steward Johnston & Reens
986 Bedford Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: St. Onge Steward Johnston & Reens
STRRET: 986 Bedford Street
APPLICANT: Susan Hockfield
APPLICANT: Diane M. Javorski
TITLE OF INVENTION: BEHAB, A Brain Hya-
TITLE OF INVENTION: luronan-Binding Protein
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application PC/TUS9504353
GENERAL INPORMATION:
APPLICANT: Susan Hockfield
APPLICANT: Diane M. Jaworski
TITLE OF INVENTION: BEHAB, A Brain Hya-
TITLE OF INVENTION: 1 Luronan-Binding Protein
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DESCRIPTION: DNA encoding a protein
                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" 1.44 Mb diskette
COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                                                        US/08/225,477B
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MEDIUM TYPE: 3.5" 1.44 Mb diskette
                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: MS DOS
SOFTWARE: Word Processor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/22:
FILING DATE: APTIL 8, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FRAGMENT TYPE: entire sequence
IMMEDIATE SOURCE: rat brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 203-324-6155
TELEFAX: 203-327-1096
                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: MALY M. Krinsky
REGISTRATION NUMBER: 32423
REFERENCE/DOCKET NUMBER: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 203-327-1096
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 CCACGCGCCAAAGGCCGGG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ctacccggccgaaggccggg 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: MS DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Word Processor CURRENT APPLICATION DATA:
                                                                                                                                                                                                                 United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1520 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      United States
                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: rat BEHAB
                                                                                                                                       STREET: your
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stamford
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FRAGMENT TYPE:
                                                                                                                                                                                                                                     06905
                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U
ZIP: 06905
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PCT-US95-04353-1
                                                                                                                                                                                                                 COUNTRY:
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NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                                                                                                          RESULT 10
US-08-457-797A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER
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APPLICANT: SZYÍ, MOSHE
APPLICANT: BIGGY, PASCAL
APPLICANT: BIGGY, PASCAL
APPLICANT: BAGGY, PASCAL
APPLICANT: RAIChANDAN METHYLTRANSFERASE GENOMIC SEQUENCES AND ANTISENSE
TITLE OF INVENTION: DIA METHYLTRANSFERASE GENOMIC SEQUENCES AND ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES
FILE REFERENCE: 106101.194
CURRENT FILING DATE: 1999-06-24
CURRENT FILING DATE: 1997-12-17
EARLIER PELLING DATE: 1997-12-17
EARLIER FILING DATE: 1997-05-30
NUMBER OF SEQ ID NOS: 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
                                                             GENERAL INFORMATION:
APPLICANT: Sayf, Moshe
APPLICANT: Bigey, Pascal
APPLICANT: Ramchandani , Shyam
APPLICANT: Ramchandani , Shyam
TITLE OF INVENTION: DNA METHYLTRANSFERASE GENOMIC
TITLE OF INVENTION: SEQUENCES AND ANTISENSE OLIGONUCLEOTIDES
NUMBER OF SEQUENCES: 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.0%; Score 14.8; DB 3; Length 254; 88.9%; Pred. No. 2.18+02; Aative 0; Mismatches 2; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/866,340
                                                                                                                                                                                                                                                                                                                                 United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-103-875-37/c
; Sequence 37, Application US/09103875A
; Patent No. 6221849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: other nucleic acid HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
US-08-866-340-31/c
; Sequence 31, Application US/08866340
; Patent No. 6020318
                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: HALE AND DORR LLP
STREET: 60 State Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: KEOMN, WAYNE A.
REGISTRATION NUMBER: 33,923
REFERENCE/DOCKET NUMBER: 106
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (617) 526-6000
TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 31.
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 254 base pairs TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                   02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                                                               STATE:
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/codon_start= 64
/function= "chitinase"
/product= "26 kD preprotein of chitinase G (ChiG)"
/note= "antifungal activity, especially on
/richoderma reesii and Fusarium sporotrichoides as
well as Rhizoctonia solani and Botrytis cinerea."
                                                                                                                                                                                                                     ö
                                                                                                                                                                      74.0%; Score 14.8; DB 4; Length 254; 88.9%; Pred. No. 2.1e+02; tive 0; Mismatches 2; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Transgenic pathogen-resistant organism NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARRENT APPLICATION
APPLICATION WINBER: US/08/457,797A
FILING DATE: June 1, 1995
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 18,839
REGISTRATION NUMBER: 35,225
REGISTRATION NUMBER: 35,225
REGISTRATION NUMBER: 35,225
REFERENCE/DOCKET NUMBER: A29542 FWC - 37/31335
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 408-2500
TELEFAX: (212) 765-2519
TELEFAX: (212) 765-2519
SEQUENCE CHARRATERISTICS:
LENGTH: 1002 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Brumbaugh, Graves, Donohue and Raymond STREET: 30 Rockefeller Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/08457797A patent No. 5689045 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Hordeum vulgare
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                                                                                                                                                                                                                                                                                                                  66 ACCAGGCCCAAGGCCGGG 49
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 37
LENGTH: 254
                                                                                                                                                                                                                            Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
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862..1002
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                      ; TYPE: DNA
; ORGANISM: HOMO sapiens
US-09-103-875-37
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                                                                                                                                                                               Query Match
Best Local Similarity
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LOCATION: 1..63
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: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
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OTHER INFORMATION: /partial OTHER INFORMATION: /note= "11 nucleotides at 3' end not shown"
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Pred. No. 1.9e+02;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Transgenic pathogen-resistant organism NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                             NAME/KEY: polyA_signal
LOCATION: 95..910
OTHER INFORMATION: /note="potential polyadenylation
OTHER INFORMATION: signal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                          NAME/KEY: sig_peptide
LOCATION: 298..312
OTHER INFORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: sig_peptide
LOCATION: 466..588
OTHER INFORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
                                                                                                                                                                                                                 /note= "probable signal peptide
sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: /note= "probable signal peptide OTHER INFORMATION: sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: /note= "probable signal peptide OTHER INFORMATION: sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Brumbaugh, Graves, Donohue and Raymond STREET: 30 Rockefeller Plaza
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; Patent No. 5804184
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NAME: Tenser, Arthur
REGISTRATION NUMBER: 18,839
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88.9%;
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MEDIUM TYPE: Floppy disk
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Best Local Similarity 88.99
Matches 16; Conservative
                                                                                                                                                                   NAME/KEY: Sig_peptide LOCATION: 64..294 OTHER INFORMATION: /nc OTHER INFORMATION: Sec
                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: sig_peptide
LOCATION: 349..378
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LOCATION: 607..861
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LOCATION: 133..861
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STATE: New York
COUNTRY: U.S.A.
ZIP: 10112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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US-08-457-797A-9
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US-08-812-025-9
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/codon_start= 64
function= "chitinase"
function= "chitinase"
forduct= "26 kD preprotein of chitinase G (ChiG)"
forde= "antifungal activity, especially on
Trichoderma reesii and Fusarium sporotrichoides as
well as Rhizoctonia solani and Botrytis cinerea."
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OTHER INFORMATION: /partial
OTHER INFORMATION: /hote= "11 nucleotides at 3' end not shown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: sig_peptide
LOCATION: 64..294
OTHER INFORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 298.312
OTHER INFORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
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LOCATION: 319..378
COTHER INFORMATION: Sequence" probable signal peptide
OTHER INFORMATION: sequence"
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                                              A29542 FWC - 37/31335
                                                                                   TELEPHONE: (212) 408-2500
TELEFAX: (212) 765-2519
TELEX: 23855
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1002 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
NAME: Kole, Lisa
REGISTRATION NUMBER: 35,225
                                         REFERENCE/DOCKET NUMBER: A21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 408-2500
                                                                                                                                                                                                                                                                                                                                   Hordeum vulgare
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Matches 16; Conservative
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LOCATION: 466..588
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LOCATION: 607.861
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133..861
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OTHER INFORMATION:
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LOCATION: 1..63
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                     STRAIN: L.
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US-08-812-025-9
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GENERAL INCREMATION:
GREAT INCRAMATION:
GREAT INCRAMATION:
APPLICANT: Puncting, Michaeline
APPLICANT: Tang, Wen
APPLICANT: Topham, Matthew
TITLE OF INVENTION: Matchew
FILLE REFERENCE: 2037.2.1a
CURRENT APPLICATION NUMBER: US/08/841,483B
CURRENT FILING DATE: 1997-04-22
EARLIER FILING DATE: 1997-04-22
SAFLIER FILING DATE: 1997-04-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VET: 2.0
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Pred. No. 1.9e+02;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 607.861
OTHER INFORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
                                                                                                           NAME/KEY: sig_peptide
LOCATION: 298..312
OTHER INFORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
                                                                                                                                                                                                                                                             NAME/KEY: sig_peptide
LOCATION: 349..378
OTHER INFORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: sig_peptide
LOCATION: 466..588
OTHER INFORMATION: /note= "probable signal peptide
OTHER INFORMATION: sequence"
/note= "probable signal peptide
sequence"
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; Patent No. 5976875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3255 ACCCGGCCGAAGACCAGG 3238
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88.9%;
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Best Local Similarity 88.9
Matches 16; Conservative
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Best Local Similarity 88.9
Matches 16; Conservative
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) LOCATION: 133..861
US-09-138-873A-9
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US-08-841-483-3
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ORGANISM: Homo sapiens
LOCATION: 64..294
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
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US-08-841-483-3/C
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LENGTH: 3490
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/function= "chitinase"
/product= "26 kD preprotein of chitinase G (ChiG)"
/product= "antifungal activity, especially on
/richederma reesii and Fusarium sporotrichoides as
well as Rhizoctonia solani and Botrytis cinerea."
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OTHER INFORMATION: /partial
OTHER INFORMATION: /note= "11 nucleotides at 3' end not shown"
                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Transgenic pathogen-resistant organism NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER FLAINABLE FLOWER:

MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC Compatible
COMPUTER: TEM PC Compatible
COMPUTER: TEM PC COMPATIBLE
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U4, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Tenser, Arthur
REGISTRATION NUMBER: 35,225
REFERENCE/DOCKET NUMBER: 35,225
REGIOUR CANADION: 3
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LOCATION: 905..910
OTHER INFORMATION: /note="potential polyadenylation
OTHER INFORMATION: signal"
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                                                                                                                                                                                                                                          US-09-138-873A-9; Sequence 9, Application US/09138873A; Patent No. 6271438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Baker & Botts
STREET: 30 Rockefeller Plaza
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Hordeum vulgare
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 10112
COMPUTER READABLE FORM:
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OTHER INFORMATION:
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: U.S.A.
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LOCATION: 1..63
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APPLICANT:
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APPLICANT: Prescott, Steven M.
APPLICANT: Prescott, Steven M.
APPLICANT: Prescott, Michaeline
APPLICANT: Tang, Wan
APPLICANT: Tang, Wathew
TITLE OF INVENTION: Diacylglycerol Kinase Isoforms Epsilon and Zeta and
TITLE OF INVENTION: Methods of Use Thereof
TITLE OF INVENTION: Methods of Use Thereof
TITLE OF INVENTION: Methods of Use Thereof
TITLE OF INVENTION: MABER: US/09/382,911
CURRENT FILING DATE: 1999-08-25
PRIOR FILING DATE: 1997-04-22
PRIOR PILING DATE: 1996-04-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATCH IN VEY: 2.0
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US-08-841-483-5/c

| Sequence 5, Application US/08841483B |
| Patent No. 5976875 |
| GENERAL INPORMATION: |
| APPLICANT: Prescott, Steven M. |
| APPLICANT: Topham, Matthew |
| APPLICANT: Topham, Matthew |
| TITLE OF INVENTION: Methods of Use Thereof |
| FILE REFERENCE: 2037.2.1a |
| CURRENT FILING DATE: 1997-04-22 |
| BARLIER FILING DATE: 1996-04-22 |
| NUMBER OF SEQ ID NOS: 33 |
| SOFTWARE: PatentIn Ver. 2.0 |
| SOFTWARE: PatentIn Ver. 2.0 |
| Control of the control of t
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                                         Sequence 3, Application US/09382911
Patent No. 622168
: GENERAL INFORMATION:
: APPLICANT: Prescott, Steven M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 3255 ACCGGCCGAAGACCAGG 3238
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Best Local Similarity 88.9%
Matches 16; Conservative
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; LOCATION: (126)..(3479)
US-08-841-483-5
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ORGANISM: Homo sapiens
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; LOCATION: (89)..(2875)
US-09-382-911-3
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ORGANISM: Homo sapiens
US-09-382-911-3/c
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LENGTH: 4094
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SEQ ID NO 3
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Search completed: June 19, 2002, 15:49:00 Job time: 13798 sec

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June 19, 2002, 14:04:08; Search time 7489.97 Seconds (without alignments) 36.040 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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27472414 13736207 seqs, 6748477542 residues Total number of hits satisfying chosen parameters:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

Scoring table:

Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

em\_gss\_hum:\* em\_gss\_inv:\* em\_gss\_pln:\* em\_esthum:\* em\_estin:\* em\_estmu: em\_estpu: em\_estpl: em\_estro: em\_htc:\* gb\_estl:\* em\_estba:\* gb\_est2:\* qb\_htc:\* \*:ssb\_dp ESI:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em\_gss\_vrt:\*

BE260627 601146118 BM467912 AGENCOURT BG320293 ZM03\_1281 BF286795 EST451386 B18042 A-237G3.TV B1779841 EBEM07\_SQ B1779842 EBEM07\_SQ AW142153 EST292377 BG298646 60236847 BM376491 EBEM05\_SQ BM376491 EBEM05\_SQ BM376491 EBEM05\_SQ BM376491 EBEM05\_SQ BM376491 TV C BE114196 UI-R-CAO-BE238940 MD0596 Me BF679019 602153663 BE114197 UI-R-CAO-AL539606 AL539606 Description BE114196 SUMMARIES BE114197 BE114196 BE238940 BF679019 BM467932 BG320293 BF286795 BM376491 B18122 BG417064 BI779841 BI779842 BE260627 BG298646 AL539606 AW142153 0 12 Match Length DB 885.0 885.0 882.0 779.0 779.0 779.0 779.0 Score 115.8 115.8 115.8 115.8 115.8 115.8 16.8 16.4 16.4 16.4 16.4 Result 7 8 8 10 11 11 13 ٠ و υυ 000

AW919607 EST350911 BG846215 102401260 BF103096 601646433 AG093531 Pan trog1 BG846216 102401260 BE454137 HVSMEh008 BG181627 RST477 At B1908420 603067366 AZ210881 SP_0153_B AL220563 Tetraodon BF791915 60103378 AL166592 Terraodon BF791915 601585811 AG086086 Pan trog1 AG086086 Pan trog1 AAC83327 RTH084 HT BB571165 BB571165 AW333768 WK96605.x HH813476 BB571165	m	BB697893 BB697893 BH353262 CH230-68L BH54931B BGCNU671R BM439271 GIT000007 BI559944 603253407 AI963704 wr64h07.x
9 AW919607 10 BG846215 12 AGC093531 12 BCG093531 10 BE46216 10 BE454137 10 BE454137 10 BC9420 12 AZ210881 12 CNS02261 12 CNS02261 10 BF78027 12 CNS01TTB 11 BF78027 12 AGC086086 9 AA33127 9 BB571165 9 AW3134768	9 AA997260 10 BM199463 9 AW619475 9 AW916542	9 BB69/893 12 BH353262 12 BH349318 10 BM439771 10 BI559944 9 AI963704
552 552 669 678 678 876 876 909 909 900 11156 1114 1144 1144 1332 332	416 417 478	483 500 617 640 685 717
79.0	77.0	77.0 77.0 77.0 77.0 77.0
155.88	15.4	15. 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
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# ALIGNMENTS

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EST 13-JUN-2000
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                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                1 (bases 1 to 448)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                              BE114197
UI-R-CAO-axo-b-10-0-UI.sl UI-R-CAO Rattus norvegicus cDNA clone
UI-R-CAO-axo-b-10-0-UI 3', mRNA sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
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/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: msoares@blue.weeg.uiowa.edu
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                                                                                                                                                                                                                                                                                                                                                                                              Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                       BE114197.1 GI:8506302
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                                                                                                                                                                                   Norway rat.
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KEYWORDS
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TITLE
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RESULT
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/clone="II-R-CA0"
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/note="Vector: pT7130-pac (Pharmacia) with a unrecomposition of the observable in the plantary is a subtract corresponded description of the library from which this clone was derived, please visit our web site at ratest.eng.ulowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares,
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CAO library is a subtracted library derived from the following tissues: thalamus, cerebellum, hypothalamus, medula, pons tissues; thalamus, cerebellum, hypothalamus, medula, pons hippocampus. For a detailed description of the library from which this clone was derived, please visit our web site at ratest.eng uitowa edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)

TAG_SEC=None found:
88 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 491)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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Fax: 319 335 9565
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                                                                                                                                                                                                                                                                                                                                                                                   85.0%; Score 17; DB 9; Length 448; 100.0%; Pred. No. 1.3e+03; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
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/organism="Rattus norvegicus"
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Seg primer: M13 Forward
POLYA-No.
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97044477
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/db_xref="taxon:10116"
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Best Local Similarity 100.0
Matches 17; Conservative
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linear EST 11-JUL-2000
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Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.
                                                                                                                                                                                                                                                                                                                                             BE238940 612 bp mRNA linear EST 11-JUL-2
MD0596 Meloidogyne incognita J2 (#MD99-1) Meloidogyne incognita
cDNA clone 3438 5' similar to SEC-2 protein (Y09293), mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 612)
Dautova, M., Gommers, F.J., Bakker, J. and Smant, G.
Dautova, M., Gommers, F.J., Bakker, J. and Smant, G.
S' end expressed sequence tags from Meloidogyne incognita
preparasitic J2 cDNA library
Unpublished (2000)
Contact: Smant G / Dautova M
Laboratory of Nematology
Wageningen University and Research Center
Box 8123, Binnenhaven 10, 6709 PD Wageningen, The Netherlands
Tel: 31 317 485 254
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Best Local Similarity 90.0%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                     Score 17; DB 9; Length 491;
Pred. No. 1.3e+03;
                                          1 others
                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Meloidogyne incognita"
/db_xref="taxon:6306"
Genome Research 6:791-806, 1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Std Error: 0.00
                                          92 t
                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Insert Length: 612 Std Error:
Seq primer: T7 promoter primer
High quality sequence stop:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 southern root-knot nematode.
                     TAG SEQ-None found"
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                                                                                                                            85.0%;
100.0%;
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                                                                                                                                                                                                                                                   32 CCCGGCCGAAGGCCGGG 48
                                                                                                                                                 Best Local Similarity 100.0
Matches 17; Conservative
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/clone_lib="NIH_MCC_83"
/lab_host="NIH_MCC_83"
/lab_host="DHIOB (TI phage-resistant)"
/noce="Organ: prostate; Vector: pDNR-LIB (Clontech);
Site_1: Sfil (gqcgcctcggcc); Site_2: Sfil (gqccattatggcc); Site_1: Sfil (gqcgctctggcc); Site_2: Sfil (gqccattatggcc); Site_1: Sfil (gqcgctctggcc); Site_2: Sfil (gqccattatggcc); Site_1: Sfil (gqcgctctggcc); Site_3: Sfil (gqccattatggcc); Site_1: Sfil (gqccattatggcc); Site_3: Sfil (gqccatt
       #602153663F1 NIH_MGC_83 Homo sapiens cDNA clone IMAGE:4294839 5',
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                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 786)
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1 (bases 1 to 849)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-Length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.m column: 16
High quality sequence stop: 564.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Gapbs-rémail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
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Pred. No. 2.4e+03;
0; Mismatches 1; Indels 0;
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/db_xref="taxon:9606"
786 bp
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AL539606
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Best Local Similarity 94.4'
Matches 17; Conservative
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                                                                  mRNA sequence.
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/clone="CSODF058TD18"
/clone_lib="LTI_FL013_FBrn1"
/dev_stage="pooled tissue from post conception fetuses (20
week, 24 week and 26 week)"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                 //Octe="Ocgan: Fetal brain; Vector: pcwVSPORT 6; 1st strand CDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMVSPORT 6 vector. Library was constructed by Life Technologies. Contact: Feng Library Technologies. Contact: Feng Library Econologies, a division of Invitrogen 9800 Medical Center Drive Rockville invitrogen 9800 Medical Center Drive Rockville filangellifetech.com URL:

http://fullmagellifetech.com URL:

187 c 267 g 205 t 1 others
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/lab_host="HH10B (phage-resistant)"
/note="Corgan: brain, Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Library constructed by Ling Hong
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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601146118F1 NIH_MGC_19 Homo sapiens cDNA clone IMAGE:3161405 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G. E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM119 row: c column: 06
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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85.0%; Pred. No. 2.4e+03;
tive 1; Mismatches 2; Indels (
                                                                                                             /organism="Homo sapiens"
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Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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High quality sequence stop: 661.
Location/Qualifiers
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/clone_lib="NIH_MGC_19"
                                                                                                                                         /db_xref="taxon:9606
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Matches 17; Conserva
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/lab_host="DH10B (phage-resistant)"
/note="Norgan: uterus; Vector: pcMV-SPORT6; Site_1: Not1:
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.1 kb.
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AGENCOURT_6437854 NIH_MGC_71 Homo sapiens CDNA clone IMAGE:5532832
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 172)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
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CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: L.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: The I.M.A.G.E. Consortium
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov. l column: 17
High quality sequence start: 5
High quality sequence stop: 638.
Location/Qualifiers
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Pred. No. 2.4e+03;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                          0;
                                                                                                                                             Score 16.4; DB 10; Length 996;
Pred. No. 2.4e+03;
0; Mismatches 1; Indels 0:
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:5532832"
/clone_lib="NIH_MGC_71"
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Tissue Procurement: ATCC
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Matches 17; Conservative
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/Lissue_type="Leaf, crown"
/dev.stage="4-leaf, crown"
/dev.stage="4-leaf"
/note="vector: Bluescript SK+/XhoI-EcoRI; Site_1: Eco RI;
/note="vector: Bluescript SK+/XhoI-EcoRI; Site_2: Xho I;
Site_2: Xho I; Corn seedlings at 4-leaf stage were exposed
to low temperature/high light (10oC/700-800uE/m2/s) for 4
days. Plants were grown/treated by J. Simmonds/L. Cass.
Library prepared by C. Piche using Stratagene kit."
a 168 c 171 g 71 t 24 others
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Malek, R.L., Cho, J., Lee, Y., Karamycheva, S., Parvizi, B., Pertea, G., Sultana, R., Tsai, J., White, J., Quackenbush, J. and Lee, N. H. Generation of Esrs from Normalized Rat Embryo, Bento Soares Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="Zm03_12e11"
/clone_lib="zm03_AAFC_ECORC_cold_stressed_maize_seedlings"
                                                                                                                                                                                                                                                                   1 (bases 1 to 490)
Simmonds,J.A., Singh,J.A., Piche,C., Cass,L., Couroux,P., De Moors,A., Harris,L.J., Hattori,J.I., Ouellet,T., Robert,L.S., Sprott,D. and Tinker,N.A.
Expressed Sequence Tags from Cold-Stressed Maize Seedlings Grown Under High Light Intensity
Unpublished (2001)
                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Agriculture and Agri-food Canada 960 Canida Avenue, Bldg. 20, Ottawa, Ontario, KIA 0C6, Canada Tel: (613) 759-1662 Fax: (613) 759-1701
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The Institute for Genomic Research
TJC, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80.0%; Score 16; DB 10; Length 490;
80.0%; Pred. No. 3.4e+03;
tive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Singh, J.A.
Eastern Cereal and Oilseed Research Centre
cDNA clone Zm03_12e11, mRNA sequence.
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/cultivar="CO328"
/db_xref="taxon:4577"
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Location/Qualifiers
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A-237G3.TV CIT978SK Homo sapiens genomic clone A-237G3, DNA
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//cell_type="Fibroblast"
//ocll_type="Fibroblast"
//ocll_type="Vector: pBAC108L; Site_1: HindIII; Site_2: HindIII;
CalTech Human BAC Library A"
112 q 40 t 1 others
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Adams, M.D., Kelley, J.M., Rounsley, S.R. and Venter, J.C. Use of a BAC End Sequence Database for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                            /clone_lib="Rat Gene Index, normalized rat, Rattus
Fax: (301)-838-0208
Thanl: inhee@tigr.org
This clone is available through the ATCC, contact the ATCC
tel#703-365-2700 for further information.
Location/Qualifiers
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Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                       /organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="RGIFS78"
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                                                                                                                                                                                              /tissue_type="mixed tissue"
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Other_GSSs: 237G3.rp
Contact: Mark Adams
Department of Eukaryotic Genomics
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/db_xref="taxon:9606"
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/clone_lib="CIT978SK"
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79.0%; Score 15.8; DB 12; Length 313;

Query Match

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EBem07_SQ001_C21_R IGF Barley EBem07 library Hordeum vulgare cDNA
clone EBem07_SQ001_C21 5', mRNA sequence.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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Unpublished (2001)
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All sequence has a Phred quality score of 20 or over
Seq primer: M13 reverse.
89.5%; Pred. No. 4.1e+03; indels
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/clone_lib="IGF_Barley EBem07 library"
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/dev_stage="28 days post anthesis"
/lab_host="DH10B"
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Scottish Crop Research Institute
Scottish Crop Research Institute
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
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/cultivar="Optic"
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Matches 17; Conservative
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                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                  1 (bases 1 to 319)
Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardle, L.,
Barasay, L., Machray, G., Marshall, D.F.M. and Waugh, R.
Development of Barley Transcriptome Resources
Unpublished (2001)
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Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                     Email: rwaugh@scri.sari.ac.uk
All sequence has a Phred quality score of 20 or over
Seq primer: M13 reverse.
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/db_xref="textor:4513"
/clone="EBem07_S001_C22"
/clone=lib="IGF Barley EBem07 library"
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/dev_stage="28 days post anthesis"
/lab_host="DH108"
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Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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National Institutes of Health, Mammalian Gene Collection (MGC)
Email: nhlee@tigr.org
Email: nhlee@tigr.org
For clone availability, additional sequence and expression
information related to this EST please check the TIGR Rat Gene
Index (http://www.tigr.org/tdb/rgl/rgi.html). To order a clone
contact the ArCC (http://www.atcc.org/atcc.html).
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Contact: Robert Strausberg, Ph.D.
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ISM Hordeum vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae

Triticeae; Hordeum

Rassa; L. dases 1 to 438)

Ramsay, L. Machray, G., Marshall, D.F.M. and Waugh, R.

Development of Barley Transcriptome Resources

M. Unpublished (2001)

Contact: Waugh R

Unit of Genomics

Scottish Crop Research Institute

Invergourie, Dundee, D2 5DA, Scotland, UK

Tel: 00 44 1382 562426

Fax: 00 44 1382 562426
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                                                                                                                                                                                                                                                           EST 10-JAN-2002
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                                                      0; Gaps
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79.0%; Score 15.8; DB 10; Length 426; 89.5%; Pred. No. 4.2e+03; tive 0; Mismatches 2; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: rwaugh@scri.sari.ac.uk
All sequence has a Phred quality score of 20 or over
Seq primer: M13 reverse.
Location/Qualifiers
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/clone="EBem05_SQ002_G02"
/clone_lib="IGF Barley EBem05 library"
/tissue_type="Embryo"
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/lab_host="DH10B"
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AJ132187 faba bean AJ005966 faba bean AR063452 Sequence L32167 Banana bnc AR063453 Sequence

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AJ005964 faba bean AJ132345 Nanovirus AR145398 Sequence UIG735 Subterranea AR145394 Sequence UIG731 Subterranea AB009047 Milk vetc

AR010230 Sequence AR112007 Sequence AR010227 Sequence U18077 Banana bunc AR010225 Sequence AR010240 Sequence

AF102780 Banana bu AF416465 Banana bu S56276 orf V1 {com R010232 Sequence AF416469 Banana bu

AJ238493 Nanovirus AJ132344 Nanovirus

AR010234 Sequence AF416464 Banana bu AR010229 Sequence AF416467 Banana bu

PAT 17-DEC-2001

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No. Result

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Rohde,W., Becker,D., Randles,J.W., Hehn,A. and Salamini,F.
Use of a virus DNA as promoter
Datent: US 6303345-A 1 16-OCT-2001;
Location/Qualifiers
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        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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88.5%; Scor.
100.0%; Pred. No. ...
0; Mismatches
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         /note="stem-loop structure"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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/db_xref="G1:323311"
                                                                                                                                                                                        /codon_start=1
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/db_xref="G1:323308"
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/db_xref="G1:323310"
                                                         /protein_id="AAA42894.1"
/db_xref="GI:323307"
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/note="ORF 4"
                                                                                                                                                                                                                                                                                               /codon_start=1
                                /note="ORF 1"
                                                 /codon start=1
                                                                                                                                                                                                                                                                                                                                                                       /note="ORF 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="ORF 5"
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Coconut foliar decay virus DNA, clones NMORG, poRG, and poRGSAU3

Coconut foliar decay virus

Viruses; ssDNA viruses; Nanovirus.

I (bases 1 to 1.29.1)

Rohde, W., Randles, J.W., Langridge, P. and Hanold, D.

Nucleotide sequence of a circular single-stranded DNA associated with coconut foliar decay virus

Virology 176, 648-651 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1021 TATCGTTTACATCTTATGAATATCCTGCCCAGGCCGAAGGCCTGGGAGGTGCTACCCGGC 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agggcattcagttcggacaaatacgaaccccttagttatcttgggttcgaccatgtgcat 300
                                                                                                                                                                                                                                                                                                  ctgtggaatatttaaagtatgtgtcatctaaattacaccaatacccgcccacgcgc 420
                                                                                                                                                                                                                                                                                                                                                                                        421 tatcgtttacatcttatgaatatcctgcccaggccgaaggcttgggaggtgctacccggc 480
                                                                                                                                                                                                                                                                                                                                                                                                                                            cgaaggccgggaacaatatgaatcgagttatgggcgggcccacaataaaagattccattt 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ggataagaacgaatctgttactttgcttgcagtgcacgcaaccactttccacgtcaccaa 600
                                                                                                                             121 ggaaccagaaaggacgtattgtaccagtacatcgaggacccaaaacgaaatttaatcctc 180
                                                                                                                                            gtactcgtatttgccaatgtcctgcctgattatttgaaaatcagcagggacagaataaaa 360
                                                                                          gggaagteegtgtttgeeaaatateteggaeteaageeegaetggttetaeaatgtggt 120
                          1 ateggagagagagagaegategeacaateetetggatatgeggaegagaeggaggagae 60
 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Draft entry and printed sequence for [1] kindly submitted by W.Rhode, 15-MAR-1989, for release after publication. Location/Qualifiers
                                                                                                                                                                                 gatgtacccaggtgtaatttagagtatttaaattatgccctgttagaatgtgttaagaac
                                                                                                                                                                                                                                               781 GATGTACCCCAGGTGTAATTTAGAGTATTTAAATTATGCCCTGTTAGAATGTGTTAAGAAC
 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Coconut foliar decay virus"
/db_xref="taxon:12474"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coconut foliar decay virus, complete genome.
M29963
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  Mismatches
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  Conservative
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    Matches
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/translation="MTGFTWSRPVVPTNRIETTVRRNGCFSSTESRLVLESKGHDWPN DLIRNLMNDAMKTQADTEDALYTELRNNGQDGPLKTRSHFHTTIGSLKCCLRSESQRT IAQSSGYADETETGSPCLPNISDSSPTGSTHVVEPERTYCTSTSRTQNEI" complement (422. .568)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAA42899.1"
/db_xref="GI:323312"
/translation="MNRVMGGPTIKDSIWIRTNLLCLQCTQPLSTSPIQVSSLLEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MRTRRREVEVCQISRTQARLVLHMWWNQKGRIVPVHRGPKTK FNPRCTQV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MTHTLNIPQFYSVPADFQIIRQDIGKYEYMHMVEPKITKGFVFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
/translation="MGSSIRRMCFTLNYETEBEAANVVRRIESLNLVYAIVGDEVAPS
TGQRHLQGFIHLKTGRRLQGLKTVLGNDRIHLEPTRGSDEGNBYCGSKERVLLEHGVP
TREVWRRPRAAQRFAEEDBLLLEDGGSTRRCVVHGASVEWTRMAAENPFPFYKHWW
LEVLSAIGBFADDRTTLWICGRDGGDGKSVPRKYLGIKEDWRYTGGGFRKDVLLYQYIE
DPKRNLILDVPRCNLEYLNYALLECVKNRAFSSDKYEPLSYLGFBHVHVLVFANVLPD
                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MEMGTDFQRPILSIPPKLRVQRIFGIRLGLPGGVHQVPQQIVGPIVAF"
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Pred. No. 7.2e-191;
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/translation="MSAVNWVFTLNFAGEVPVLSFDERVQYAVWQHERVNHDHIQGYI
QLKKRAKMNTVKNIIGGNPHLEKMKGSIEEAGAYAQKEESRVAGPWSYGELLKKGSHK
RY IMELIKOPDENELEEPQKYRRAMADLESRSTABEGGEFYTLYSWOETVLGLLEE
EPNDRIIIWYG POWBECKSOFTGKRAKUSKRYLYLPGGKTQDMTYMLMKNPKANVYMD
IPRCNSEYLNYQFMELIKNRTIFSYKYEPVGCIINNKHHYIVLANVLPPDYEKISQDRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             circular VRL 13-JAN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  545 TAGAAGAAGACCCAATGACCGTATTATTATTTGGGTCTACGGCCCAAATGGTAACGAAG 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 ggaagteegtgtttgeeaaatateteggaeteaageeegaetggttetaeaaatgtggtg 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gggcattcagttcggacaaatacgaaccccttagttatcttgggttcgaccatgtgcatg 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 atgtacccaggtgtaatttagagtatttaaattatgccctgttagaatgtgttaagaaca
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                                                                                /function="replication-associated protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 14.9%; Score 116.4; DB 14; Best Local Similarity 57.0%; Pred. No. 6.5e-23; Matches 213; Conservative 0; Mismatches 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          faba bean necrotic yellows virus C9 gene.
AJ005966
AJ005966.1 GI:3550532
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                                                                                                                                                                                                                                                                                                                                                                                                          4
                                                                                                                                                 /product="Rep_protein"
/protein_id="CAB44027.1"
/db_xref="G1:4995172"
/db_xref="SPTREMBL:Q9WIK2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                faba bean necrotic yellows virus. faba bean necrotic yellows virus Viruses; sabNA viruses; Nanovirus.
                                                                                                                                      /evidence=experimental
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                                                                                                   /note="32.53 kDa"
                                                                                                                                                                                                                                                                                                                                                                                                        227
/3 .1003
/gene="C9-Eg"
73 .91e
                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                /gene="C9-Eg"
998. .1003
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/gene="C9-Eg"
                                                                 /gene="C9-Eg"
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Katul, L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ten distinct circular ssDNA components, four of which encode putative replication-associated proteins, are associated with the data bean necrotic yellows virus genome
J. Gen. Virol. 79 (Pt 12), 3101-3109 (1998)
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                                                                                                                                                             Timchenko, T., de Kouchkovsky, F., Katul, L., David, C., Vetten, H.J. and Gronenborn, B.
241 agggcattcagttcggacaaatacgaaccccttagttatcttgggttcgaccatgtgcat 300
                                                                       gtactcgtatttgccaatgtcctgctgattatttgaaaatcagcagggacagaataaaa 360
                                                                                                    901 GTACTCGTATTTGCCAATGTCCTGCCTGATTATTTGAAAATCAGCAGGACAGAATAAAA 960
                                                                                                                                        tatcgtttacatcttatgaatatcctgcccaggccgaaggcctgggaggtgctacccggc 480
                  cgaaggccgggaacaatatgaatcgagttatgggcgggcccacaataaaagattccattt 540
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faba bean necrotic yellows virus.
faba bean necrotic yellows virus.
viruses; ssDNA viruses; Nanovirus.
1 (bases 1 to 1007)
Katul,L., Timchenko,T., Gronenborn,B. and Vetten,H.J.
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J. Virol. 73 (12), 10173-10182 (1999)
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/db_xref="taxon:59817"
/lab_host="Vicia faba"
1. .39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        661 tttgcgcgatcggacggctgagttgatctgg 691
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Direct Submission
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BYTV2 1096 bp DNA linear VRL 30-OCT-1994 Banana bunchy top virus (BBTV DNA II) V1, V2, C1 and C2 genes,
                                                                                                                1 (bases 1 to 1096)
Wu,R.-Y., You,L.-R. and Soong,T.-S.
Nucleotide sequence of two circular SSDNA associated with banana bunchy top virus and method for detection of banana bunchy top
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       791 AGAGTITTAATAAATACAAAATACGAACCATGTGTGATTAGAAAAGATGGACAAAATGTC 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298 catgtactcgtatttgccaatgtcctgcctgattatttgaaaatcagcagggacagaata 357
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/db_xref="taxon:12585"
1. .7
                                                                                                                                                                                                                                                                                                                                                               14.6%; Score 114.2; DB 6;
illarity 57.5%; Pred. No. 2.9e-22;
Conservative 0; Mismatches 163;
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associated with banana bunchy top virus
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1 (bases 1 to 1096)
                                                                                                                                                                                                               Patent: US 5846705-A 4 08-DEC-1998;
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Banana bunchy top virus DNA.
Banana bunchy top virus
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1. .1096
                                                                                                                                                                                                                                                                          /organism="unknown"
231 c 244 g
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AR063452.1 GI:5992760
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OLKKKAKMNTVKNIIGGNPHLEKMKGSIEEASAYAQKEESRYAGFWSYGELKKGSHK
KYMELIKPDENELEEPQKYRRAMAMSAMDESRKLAEEGGFPVMFYSWGFULGLLEE
EPNDRTIIWYGPNGNEGKSOFGKFLGLKKPYLYLPGGKTQDMTYMLMKNPKANVVMD
IPPRCNSEYLNYQFMELIKNRTIYSYKYEPVGCIINNKIHVILANVLEDYEKISQDRI
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0
                                                                                                                                                                                                                                                                                                                                                                                             /function="putative replication associated (rep) protein"
Submitted (06-MAY-1998) Katul L., Institute fuer Biochemie und Pflanzenvirologie, Biologische Bundesanstalt fuer Land- und Forstwirtschaft, Messeweg 11 - 12, 38104 Braunschweig, GERWANY 2 (bases 1 to 1004)
TRALILL., Timchenko,T., Gronenborn,B. and Vetten,H.J. Ten distinct circular ssDNA components, four of which encode putative replication-associated proteins, are associated with the flab bean necrotic yellows virus genome
J. Gen. Virol. 79 (Pt 12), 3101-3109 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 gaaccagaaaggacgtattgtaccagtacatcgaggacccaaaacgaaatttaatcctcg 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 665 GTAAAACCCAAGATATGACATATGTTAATGAAAAATCCAAAGGCAAATGTTGTGATGG 724
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    1004
/organism="faba bean necrotic yellows virus"

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/proteln_id="CAA06789.1"
/db_xref="G1:3550533"
/db_xref="SPTREMBL:091252"
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DEFINITION Sequence 4 from patent US 5846705.
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                                                                                                                                                                                                                                                                                               db_xref="taxon:59817"
                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                       /isolate="SV292-88"
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56.78;
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73. .918
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PAT 29-SEP-1999
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                                                                                                                                                                                                                                                                                       1 (bases 1 to 1091)
Mu.R.-Y, You, L.P.R. and Soong/T.-S.
Nucleotide sequence of two circular SSDNA associated with banana bunchy top virus and method for detection of banana bunchy top
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gatgtacccaggtgtaatttagagtatttaaattatgccctgttagaatgtgttaagaac 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 gggaagtecgtgtttgccaaatateteggaeteaageeegaetggttetaeaatgtggt 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            666 GCAAAGACGTCGGATATGATGCACATCATAACGATGGATCCTGATAATCATTGGATATT 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    786 AGAGITITAATAAAATACAAAATACGAACCATGTGTGATTAGAAAAGATGGACAAAATGTC 845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         606 GGAAAGTCAACCTTCGCAAGATATCTATCATTAAAACCTGGATGGGGATATATCAACGGT 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             726 GATATCCCCAGAAGTCATTCAGATTATCTGAATTATGGCGTTATAGAACAAATTAAGAAT 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 agggcattcagttcggacaaatacgaacc---ccttagttatcttgggttcgaccatgtg 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         298 catgtactcgtatttgccaatgtcctgcctgattatttgaaaatcagcagggacagaata 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              846 CATGTAATTGTTATGGCAAATGTGTTGCCTGATTATTGTAAAATTTCAGAAGATAGAATA 905
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 6; Length 1091;
                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.4%; Score 112.6; DB 6; 57.3%; Pred. No. 8.5e-22; Live 0; Mismatches 164;
                                                                                                                                             DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                                                                                                                                                                                                    Patent: US 5846705-A 5 08-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   276
                                                                                                                                     Sequence 5 from patent US 5846705
AR063453
           358 aaactgtggaatatttaaagtatgtgtcatc 388
                                 911 AAAATAATTAATTGTTGAGAAAGGAAACTTC 941
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1 (bases 1 to 1095)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="unknown"
224 c 248 q
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1. .1091
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Banana bunchy top virus
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GSKKRKLLDRFRESPEELKMDDPSKYRRCLAVESIKDARINSEWVHELKEWQNKLIOH
                                                                                                                                                 /translation="MSSFKWCFTLNYSSAAEREDFLALLKEEDVHYSVVGDEVAPATG
                                                                                                                                                                                                        IEGVPDDRSIIWVYGPNGGEGKSTFARYLSLKPGWGYINGGKTSDMMHIITMDPDNHW
IIDIPRSHSDYLNYGVIEQIKNRVLINTKYEPCVIRKDGONYHVIVMANVLPDYCKIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AaA51429.1"
/db_xref="G1:520795"
/translation="MGLRPNKRFINYNDFLMHLMIACSASYRVGSTCFLIACGGSFLS
                                                                                                                                                                                                                                                                                                                                                                                                /translation="MVLHSELFLRSGARRLSRSSEGGCSLLCRRRSRSGHRPEAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MMCIISDVFPPLIYPHPGFNDRYLAKVDFPSPPLGPYTQMILRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           671 GGAAAGACGTCGGATATGATGCACATCATAACGATGGATCCTGATAATCATTGGATTATT 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 gatgtacccaggtgtaatttagagtatttaaatttatgccctgttagaatgtgttaagaac 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 114.2; DB 14; Length
Pred. No. 2.9e-22;
0; Mismatches 163; Indels
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                                                                                                            /protein_id="AAA51426.1"
/db_xref="GI:520792"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAA51428.1"
/db_xref="GI:520794"
                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAA51427.1"
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/gene="C1"
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57.58;
       /4. .928
/gene="V2"
71. 000
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85. .309
                                                                          /qene="V2"
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Banana bunchy top virus DNA III ORF V1 and ORF C1 genes, complete
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                                                                                                  Banana bunchy top virus
Viruses; ssDNA viruses; Nanovirus.
1 (bases 1 to 1111)
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/db_xref="G1:642392"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAA61875.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(497. .643)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="GI:642391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="ORF C1"
                                                                                       Banana bunchy top virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="ORF V1"
                                                                                                                                                                                                                                  2 (bases 1 to 1111)
Wu,R.-Y.
                                      U12586
U12586.1 GI:642390
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       DEFINITION
                                                                                                         ORGANISM
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                                        ACCESSION
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                                                                                                                                          REFERENCE
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                                                         VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IEGYPDDRSIIWVYGPNGGEGKSTFARYLSLKPGWGYINGGKTSDMMHIITWDPDNHW
IIDIPRSHSDYLNYGVIEQIKNRVLINTKYEPCVIRKDGQNVHVIVMANVLPDYCKIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MSSFKWCFTLNYSSAAEREDFLALLKEEELNYAVVGDEVAPSTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RKHLQGYLSLKKSIKLGGLKKRYSSKAHWERARGTDEQNRGYCSKETLVLELGTPVVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GSKKRKLLERFRESPEELKMEDPSKYRRCLAVESLNNARKNSEWVHELREWQNKLIQH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 gatgtacccaggtgtaatttagagtatttaaattatgccctgttagaatgtgttaagaac 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 catgiacicgiatitigccaaigiccigatiatitigaaaaicagcaggacagaaia 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ggaaccagaaaggacgtattgtaccagtacatcgaggacccaaaacgaaatttaatcctc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                604 GGAAAGTCAACCTTCGCAAGATATCTATCATTAAAACCTGGATGGGGATATATCAACGGT 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             664 GGAAAGACGTCGGATATGATGCACATCATAACGATGGATCCTGATAATCATTGGATTATT 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 agggcattcagttcggacaaatacgaacc---ccttagttatcttgggttcgaccatgtg 297
                        Additional rep-encoding DNAs associated with banana bunchy top
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                 Submitted (14-DEC-1999) School of Life Sciences, Queensland University of Technology, GPO Box 2434, Brisbane, QLD 4001, Australia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 14; Length 1095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3;
                                                                                                                                                                                                                                                                                                                                                                                                            /product="replication initiation protein"
/protein_id="AAG44004.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 112.4; DB 14; Length
Pred. No. 9.7e-22;
0; Mismatches 156; Indels
          Horser, C.L., Karan, M., Harding, R.M. and Dale, J.L.
                                                                                                         Horser, C.L., Karan, M., Harding, R.M. and Dale, J.L.
Direct Submission

    1095
/organism="Banana bunchy top virus"

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                                                             Arch. Virol. 146 (1), 71-86 (2001)
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                                                                                                                                                                                                                                            /isolate="Taiwan"
/db_xref="taxon:12585"
/note="satellite S2"
                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="GI:12004328"
                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 252 g
                                                                                                                                                                                                                                                                                                             /gene="ORF V1"
                                                                                                                                                                                                                                                                                                                                              /qene="ORF V1"
                                                                                                                                                                                                                                                                                                                                                                            /gene="ORF V1"
                                                                                                                                                                                                                                                                                                                                                                                              /codon_start=1
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nilarity 57.9%;
Conservative (
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/translation="MSSFKWCPTLNYSSAAEREDFLALLKEEELNYAVYGDEVAPSSG
OKHLOGYLSIKKSIKLGGLKKKYSSRAHWERARGSDEDNAKYCKSFTLLLEGFPASO
GRNRRALSBEWYSRSPEWHIEDPETIHTYSYKKLKKFKFEEFVHPCLDRPWGIQLTEA
IDEEPDDRTIFWYGPGNGGRSTYAKSLMKKDWFYTRGKKRNILESYVDEGSEKHI
VFDIPRCNODYLNYDVIEALKDRVIESTKYKPIKLVELNNIHVIVMANFMPEFCKISE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MTSHMLISPHYHSDHRPRRSFDHLVPRQLPPSIESAMVYRGKDE
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Wu.R.-Y. and You,L.-R.
Nucleotide sequences of DNA III and DNA IV associated with banana
bunchy top virus and their relation to other closely related virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 gggaagteegtgtttgeeaaatateteggaeteaageeegaetggttetaeacatgtggt 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       676 GGGAAGAAGAAGAACATACTGTTCTCTTACGTGGACGAAGGATCTGAGAAGCATATTGTA 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         238 aacagggcattcagttcggacaaatacgaacccttagttatcttgggttcgaccatgtg 297
                                                                                                                                                                                                                                               Direct Submission
Submitted (25-JUL-1994) Rey-Yuh Wu, Agricultural Biotechnology
Submitted (25-JUL-1994) Rey-Yuh Wu, Agricultural Biotechnology
Division, Development Center for Biotechnology, 81 Chang Hsing
Street, Taipei, 10671, Taiwan, ROC
Location/Qualifiers
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56.7%; Pred. No. 8e-18;
Live 0; Mismatches 165; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Banana bunchy top virus"
/db_xref="taxon:12585"
/clone="H-4"
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BBU12587 1127 bp DNA circular VRL 01-FEB-1995
Banana bunchy top virus DNA IV ORF VI and ORF CI genes, complete
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GSNRRKLSEMVSRSPERMRIEQPEIYHRYTSVKKLKKFKEEFYHPCLDRPWQIQLTEA
IDEEPDDRTIFWVYGPNGNEGKSTYAKSLMKKDWFYTRGGKKENILFSYVDEGSEKHI
YFDIPRCNQDYLNYDVIEALKDRVIESTKXKPIKLVELNNIHVIVMANFMPEFCKISE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bunchy top virus and their relation to other closely related virus
                                                                                                                                                                                                                                                                                                                                                         Banana bunchy top virus
Viruses; ssDNA viruses; Nanovirus.
1 (bases 1 to 1127)
Wu,R.-Y. and You,L.-R.
Nucleotide sequences of DNA III and DNA IV associated with banana
                                    856 CATGTAATTGTAATGGCTAATTTCATGCCAGAATTCTGTAAAATCTCCGAAGATAGAATA 915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (25-JUL-1994) Rey-Yuh Wu, Agricultural Biotechnology Division, Development Center for Biotechnology, 81 Chang Hsing Street, Taipei, 10671, Taiwan, ROC Location/Qualifiers
catgtactcgtatttgccaatgtcctgcctgattatttgaaaatcagcagggacagaata 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Banana bunchy top virus"
                                                                          358 aaactgtggaatatttaaagtatgtgtcatctaaa 392
                                                                                                                    916 AAGATTATTTATTGTTAAATAACACGCTATGACAA 950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/protein_id="AAA61877.1"
/db_xref="G1:642394"
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/db_xref="G1:642395"
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/note="ORF C1"
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Wu,R.-Y.
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Milk vetch dwarf virus genome segment 3 encoding virus replication-associated protein, commists and ABOAGAS.
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Sano,Y., Wada,M., Hashimoto,Y., Matsumoto,T. and Kojima,M.
Sequences of ten circular ssDNA components associated with the milk Vetch dwarf virus genome
99094638
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SHKRKIMERFEDDPEEMKIEDPSLYRRCLSRKMTEEQRSTAEWNYDMKPWODOVIQEI
BETPDYRKIIWVYGEKGGEGKSTFARYLSLKQGWGYLPGGPTHDMLHIISGEPKNNWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MPTVQSTCWVFTLNFKGEIPILPFNERVQYACWQHERVGHDHLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (08-FEB-1997) Yoshitaka Sano, Kyoto Institute of Technology, Department of Applied Biology; Matsugasaki, Sakyo-ku, Kyoto 606-8585, Japan (Tel:075-724-7764, Fax:075-724-7764)
121 ggaaccagaaaggacgtattgtaccagtacatcgaggacccaaaacgaa---atttaatc 177
                                      676 GGGAAGAAGAACATACTGTTCTCCTACGTGGACGAAGGATCTGAGAAGCATATTGTA 735
                                                                                  178 ctcgatgtacccaggtgtaatttagagtatttaaattatgccctgttagaatgtgttaag 237
                                                                                                         238 aacagggcattcagttcggacaaatacgaacccttagttatcttgggttcgaccatgtg 297
                                                                                                                                                                                       856 CATGTAATTGTCATGGCTAATTTCATGCCAGAATTCTGTAAAATCTCCGAAGATAGAATA 915
                                                                                                                                                                                                                                                  298 catgtactcgtatttgccaatgtcctgcctgattatttgaaaatcagcagggacagaata 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Oct 29, 1998 this sequence version replaced gi:3798655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="virus replication-associated protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   milk vetch dwarf virus (lab_host:Pisum sativum) DNA milk vetch dwarf virus
                                                                                                                                                                                                                                                                                                                               358 aaactgtggaatatttaaagtatgtgtcatctaaattacac 398
                                                                                                                                                                                                                                                                                                                                                                      916 AAGATTATTTATTGTTAAATAACACGCTATGACAATCGTAC 956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="milk vetch dwarf virus"
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/db_xref="GI:3798656"
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Location/Qualifiers
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/codon_start=1
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CSSEMMNYQAMEMMKNRCFASTKYRSVDLCCNKNVHLVVFANVAYDPTKISEDRIVII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MPRWQKQLNEHFYYNKDLQIYISYLQSIYSSSPSLDSSSFRMN
                                                                                                    /translation="MRISPNYLLNSRESSFILQLNYSLDMVMSSSFVLPDSVLNSLVE
REKRESSLEVACENPIRTSHI"
                                                                                                                                                                                                                                                                                                          QLKKKARFSTVKE11GGNPHVEKMKGT1EEASAYVQKEETRVAGPWSYGDLLKRGSHR
                                                                                                                                                                                                                                                                                           /translation="MACSNWVFTRNFQGALPLLSFDERVQYAVWQHERGTHDHIQGVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="SPTREMBL:Q66864"
                                                                                          /db_xref="SPTREMBL:Q66863"
                                                                                                                                                                                                                                                                           db_xref="SPTREMBL:Q66862"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="CAA56849.1"
/db_xref="GI:643117"
                                                /protein_id="CAA56848.1"
/db_xref="G1:643116"
                                                                                                                                                                                                                                   /protein_id="CAA56847.1"
/db_xref="G1:643115"
                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="orf3"
complement(716. .949)
/gene="orf3"
complement(157. .354)
/gene="orf2"
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Best Local Similarity 55.65
Matches 204; Conservative
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Submitted (03-001) L. Katul, Biologische Bundesanstalt, fuer
Land und Fortswirtschaft, Inst f Biochemie und Pflanz., Messeweg
11-12, 38104 Brannschweig, FRG
                                                                                                                                                                                                                                                                                                    181 gatgtacccaggtgtaatttagagtatttaaattatgcctgttagaatgtgttaagaac 240
                                                                                                                                                                                                                                                                                                                                     715 GACATCCCAAGAGTAGCGTCTGAGTATGTGGAATTATGGTGTATTAGAACAGGTTAAAAAT 774
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                                              Gaps
                                                                               1 atcggagagccagcggacgatcgcacaatcctctggatatgcggacgagacgaggaggac 60
                                                                                                                 535 ATAGAAGAGACCCTGATTACCGAAAGATTATAGGGTTTACGGCCCCAAAGGAGGTGAA 594
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Sequence analysis of a faba bean necrotic yellows virus DNA component containing a putative replicase gene
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     Score 95; DB 14; Length 1000;
Pred. No. 1.2e-16;
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                                              Indels
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                                              Mismatches 200;
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/isolate="SSV 292-88"
//db_xref="taxon:10239"
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/gene="orf2"
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52.9%;
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Katul, L.
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                                              Matches 228; Conservative
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AF216221 1109 bp DNA linear VRL 08-MAR-2001
Banana bunchy top virus satellite S1 replication initiation protein
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GSNRRKLSEMVSRSPERMRIEQPEIYHRYTSVKKLKKEKEEFYHPCLDRPWOJQLTEA
IDEEPDDRSIIWVYGPNGNEGKSTYAKSLMKRDWFYTRGGKKENILFSYVDEGSEKHI
VFDIPRCNQDYLNYDVIEALKDRVIESTKYKPIKLVELINIHVIVMANFMPEFCKISE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MSSFKWCFTLNYSSAAEREDFLALLKEEELNYAVVGDEVAPSSG
                                                                                                                                                                                                   Horser, C., Harding, R. and Dale, J. Banana bunchy top nanovirus DNA-1 encodes the 'master' replication
                                                                                                                                                                                                                                                                                                                                               Horser, C.L., Karan, M., Harding, R.M. and Dale, J.L. Additional rep-encoding DNAs associated with banana bunchy top
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 gggaagtccgtgtttgccaaatatctcggactcaagcccgactggttctacacatgtggt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 ggaaccagaaaggacgtattgtaccagtacatcgaggacccaaaacgaa---atttaatc 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (14-DEC-1999) School of Life Sciences, Queensland University of Technology, GPO Box 2434, Brisbane, QLD 4001,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              603 GGGAAATCAACATATGCGAAGTCAT---AATGAAGGAGGGTGGTTCTACACCAGAGGT
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="replication initiation protein"
/protein_id="AAG44003.1"
/db_xref="GI:12004326"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 180; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Banana bunchy top virus"
                                                                                                                                                                                                                                            initiation protein
J. Gen. Virol. 82 (Pt 2), 459-464 (2001)
21102983
                                                                                                                                                                                                                                                                                                                                                                                                             ch. Virol. 146 (1), 71-86 (2001) (bases 1 to 1109)
                                                                                                                                                              Viruses; ssDNA viruses; Nanovirus.
1 (bases 1 to 1109)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="putative sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="satellite S1"
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                                      (ORF V1) gene, complete cds
AF216221
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                                                                                                                        Banana bunchy top virus.
                                                                               AF216221.1 GI:12004325
                                                                                                                                           Banana bunchy top virus
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circular VRL 13-JAN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QKHLQGYVSLKKMIRLGGLKKKFGYRAHWEIAKCDDFQNRDYCTKETLISEIGAPVKK
GSNQRKIMDLYLQDPEEMQLKDPDTALRCNAKRLRIEYCSSFAVISLRPWQSELHRVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAEPDDRTIIWVYGSDGGGGKSTFAKELIKYGWFYTAGGKTQDILYMYAODPERNIAF
DVPRCSSEMMNYQAMEMLKNRVFASTKYRPVDLCVRKKVHLIVFANVSPDPTKISEDR
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Forever (06-MAY-1998) Katul L., Institute fuer Biochemie und
Pflanzenvirologie, Biologische Bundesanstalt fuer Land- und
Forstwirtschaft, Messeweg 11 - 12, 38104 Braunschweig, GERWANY
2 (bases 1 to 1004)
2 (bases 1 to 1004)
Ten distinct circular ssDNA components, four of which encode
putative replication-associated proteins, are associated with the
fibab bean necrotic yellows virus genome
J. Gen. Virol. 79 (Pt 12), 3101-3109 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /function="putative replication associated (rep) protein"
                                                                  720 TTTGATATTCCTCGCTGTAATCAGGATTATTAAATTATGATGTTATAGAGGCATTAAAG 779
                                                                                                                      298 catgtactcgtatttgccaatgtcctgcctgattatttgaaaatcagcagggacagaata 357
                                                                                                                                                                                                                                                                                                                                                                                                                                     component 1-Eg; putative; rep protein; replication
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                                        238 aacagggcattcagttcggacaaatacgaacccttagttatcttgggttcgaccatgtg
                                                                                                                                                                                                     900 AAGATTATTTATTGTTAAAAAGGAAATTATATTATGCACTATGACAATCGTACGC 954
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Pred. No. 4.5e-16;
0; Mismatches 160; Indels
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faba bean necrotic yellows virus Cl-Eg gene.
AJ005968
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/protein_id="CAA06791.1"
/db_xref="G1:3550537"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          faba bean necrotic yellows virus. faba bean necrotic yellows virus Viruses; ssDNA viruses; Nanovirus. 1 (bases 1 to 1004)
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998. .1003
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/translation="MPTLQGTFWCFTLNFSGDAPSLSFNERVQYACWQHERVSHDHLQ
GYIQMKKRSTLKMMKELLPGAHLEVSKGTPEEASDYAMKEETRVAGFWTYGELLKKGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Milk vetch dwarf virus genome segment 1 encoding viral replication-associated protein, complete sequence.
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Sano,Y., Mada,M., Hashimoto,Y., Matsumoto,T. and Kojima,M.
Sequences of ten circular ssDNA components associated with the milk vetch dwarf virus genome
J. Gen. Virol. 79 (Pt 12), 3111-3118 (1998)
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                                                                                                                                                                                                                                                                                                                                             252 ttcggacaaatacgaaccccttagttatcttgggttcgaccatgtgcatgtactcgtatt 311
                                                                                                                                                                                                                                                        192 gigtaatttagagtatttaaattatgccctgttagaatgtgttaagaacagggcattcag 251
                                                                                                                                                                                                                                                                                                                                                                                                                                 ggacgtattgtaccagtacatcgaggacccaaaacgaaatttaatcctcgatgtacccag 191
                                                                                                                                                                                                                                                                                   848 IGCAAACGIGICACCIGACCCCACAAAAIAAGIGAGGACAGAAIIGIAAIITAICAAIIG 907
                                                                                   72 gittgecaaatateteggaeteaageeegaetggitetacacatgiggiggaaceagaaa 131
                                                                                                         668 GGATATICTGTATATGTATGCTCAAGACCCAGAGAAAAATATCGCGTTCGATGTICCCAG 727
agoggacgatcgcacaatcctctggatatgcggacgagacggaggaggaggaagtccgt 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (08-FEB-1997) Yoshitaka Sano, Kyoto Institute of Technology, Department of Applied Biology; Matsugasaki, Sak
Kyoto 606-8585, Japan (Tel:075-724-7764, Fax:075-724-7764)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Oct 29, 1998 this sequence version replaced gi:3798651 Sequence updated (30-Sep-1997).

Location/Qualifiers
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/protein_id="bAA33980.1"
/db_xref="GI:3798652"
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milk vetch dwarf virus (lab_host:Pisum sativum) DNA.
milk vetch dwarf virus
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/lab_host="Pisum sativum'
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1 (bases 1 to 1007)
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                   KIASPRSILWYYGPQGGGGKTSKAKELITRGWFYTRGGKKDDVAYSYVEDPTRHVVFD
IPRDMQEYCNYSLIEMLKDRIIISNKYEPITNCQVYNIHVIVWANFLPDVTKISEDRI
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BBTV DNA II clone
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Copyright (c) 1993 - 2000 Compugen Ltd.
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## LIGNMENT

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RESULT 1
AAV71833
XX
AC AAV71833 standard; DNA; 1096 BP.
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AX AAV71833;
AC AAV71833;
AC AAV71833;
AC AAV71833;
AC AAV71833;
AS BBTV DNA II clone (2-17) nucleotide sequence.
XX
Whas bloom damage; aphid; nucleic acid detection; circular; cyclic; ss.
XX
Whas; phloem damage; aphid; nucleic acid detection; circular; cyclic; ss.
XX
XX
Banana bunchy top virus.
XX
XX
BATA_Signal 1..7

A tag a B..38
FT ATA_Signal 1..7

A tag a B..38
FT CDS
A translexcept B B..38
FT CDS
A translexcept B B..38
FT ATA_Signal A TAG B..38
FT ATA_Signal A TAG B..38
FT ATA_Signal A TAG B..38
FT A TAG
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                                                                                                                                                                                                                                                                                                                                                                                                           This represents the nucleotide sequence of a banana bunchy top virus (BBTV) DNA II (clone 2-17) circular single stranded (css) DNA. The invention provides nucleic acid sequences associated with BBTV that can be used in a PCR technique for detecting BBTV. The nucleic acid sequences (AAV71830 to AAV71833) are used as the basis for the construction of PCR primers, to detect BBTV infection. The PCR technique is used for detecting BBTV in plant tissues (preferably banana, especially Musa species). The virus, one of the most important banana species viruses, causes phloem damage and is transmitted by aphids. PCR detection gives accurate, reliable and specific determination of absence or presence of the virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              551 atcgaaggtgttcctgatgatcgaagtatcatctgggtatacggtcccaacggaggcgaa 610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gatgtacccaggtgtaatttagagtatttaaatttatgccctgttagaatgtgttaagaac 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               851 catgtaattgttatggcaaatgtgttgcctgattattgtaaaatttcagaagatagaata 910
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                                                                                                                                                                                                                                                                                               Nucleic acids having banana bunchy top virus component sequences used to design primers for use in polymerase chain reaction detection of the virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1096 BP; 347 A; 231 C; 244 G; 274 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 114.2; DB
Pred. No. 4e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aaactgtggaatatttaaagtatgtgtcatc 388
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                                                                                                                                                                   (BIOT-) DEV CENT BIOTECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.68;
57.58;
                                                                                           95US-0418071
                                                                                                                                 95US-0418071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                         Soong T, Wu R, You L;
                                                                                                                                                                                                                                               WPI; 1999-059037/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                   P-PSDB; AAW87460.
                                                                                           06-APR-1995;
                                                                                                                                 06-APR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          225;
                 US5846705-A
                                                     08-DEC-1998
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associated with banana bunchy top virus (BBTV) and the encoded proteins. Also described is a method of detecting the BBTV virus using the polymerase chain reaction (PCR). The present sequence represents a BBTV related nucleotide sequence from the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Two circular single-stranded DNAs associated with banana bunchy top
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes two circular single-stranded DNAs
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                                                                           Banana bunchy top virus related nucleotide sequence #5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1096 BP; 347 A; 231 C; 244 G; 274 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 4e-28;
                                                                                                          top virus; BBTV; detection; ds
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                                                                                                                                                                                                                                                                                                               (BIOT-) DEV CENT BIOTECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 1; 7pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.6%;
57.5%;
                                                                                                                                                                                                                                                 94TW-0106105.
                                                                                                                                                                                                                                                                                94TW-0106105.
                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 225; Conservative
                                                                                                                                                 Banana bunchy top virus
                                                                                                                                                                                                                                                                                                                                                 Wu R, You L, Song T;
                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-316145/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                               Banana bunchy
                                                                                                                                                                                                                                                 30-JUN-1994;
                                                                                                                                                                                                                                                                                  30-JUN-1994;
                                               23-AUG-2000
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             AAA38950;
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RESULT

AAA38950 standard; DNA; 1096 BP

AAA38950 ID AAA3 RESULT

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Banana bunchy top virus; BBTV; PCR technique; plant; tissue; banana;
Musa; phloem damage; aphid; nucleic acid detection; circular; cyclic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This represents the nucleotide sequence of a banana bunchy top virus (BBTV) DNA II (clone 2) and reperesents a subgenomic DNA. The invention provides nucleic acid sequences associated with BBTV that can be used in a PCR technique for detecting BBTV. The nucleic acid sequences (AAV71830 to AAV71833) are used as the basis for the construction of PCR primers, to detect BBTV infection. The PCR technique is used for detecting BBTV in plant tissues (preferably banana, especially Musa species). The virus, one of the most important banana specially wiruses, causes phloem damage and is transmitted by aphids. PCR detection gives accurate, reliable and specific determination of absence or presence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids having banana bunchy top virus component sequences used to design primers for use in polymerase chain reaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1091 BP; 343 A; 224 C; 248 G; 276 T; 0 other;
                                                                                                                      BBTV DNA II clone (2) nucleotide sequence.
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                AAV71834 standard; DNA; 1091 BP
                                                                                                                                                                                                                                                                                                                                                                                    (BIOT-) DEV CENT BIOTECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                     95US-0418071.
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                                                                                     10-FEB-1999 (first entry)
                                                                                                                                                                                                            Banana bunchy top virus.
                                                                                                                                                                                                                                                                                                                                                                                                                          You L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detection of the virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-059037/05.
                                                                                                                                                                                                                                                                                                                                                                                                                        Wu R,
                                                                                                                                                                                                                                                                                                                  06-APR-1995;
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                                                    AAV71834;
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AAV71834
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                                                                                                                                                                                                                                                                                                   666 ggaaagacgtcggatatgatgcacatcataacgatggatcctgataatcattggattatt 725
                                                                                                                                                                                                                                                                                                                                                 gatgtacccaggtgtaatttagagtatttaaattatgccctgttagaatgtgttaagaac 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           786 agagttitaataaatacaaaatacgaaccatgtgtgattagaaaagatggacaaaatgtc 845
                                                      Gaps
                                                                                   1 atcggagagccagcggacgatcgcacaatcctctggatatgcggacgagaggaggagag 60
14.4%; Score 112.6; DB 20; Length 1091; Similarity 57.3%; Pred. No. 1.4e-27; A. Conservative 0; Mismatches 164; Indels 3;
                                             224; Conservative
  Query Match
                      Best Local
Matches 22
                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                              181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 gggaagtccgtgtttgccaaatatctcggactcaagcccgactggttctacacatgtggt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      606 ggaaagtcaaccttcgcaagatatctatcattaaaacctggatggggatatatcaacggt 665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BBTV related nucleotide sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches 164; Indels
                                                                                                                                                                                                           Banana bunchy top virus related nucleotide sequence #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1091 BP; 345 A; 224 C; 247 G; 275 T; 0 other;
                                                                                                                                                                                                                                         Banana bunchy top virus; BBTV; detection; ds
                            906 aaaataattaattgttgagaaaggaaacttc 936
aaactgtggaatatttaaagtatgtgtcatc 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               virus and detection of the virus
                                                                                                                                                                                                                                                                                                                                                                                                                                      (BIOT-) DEV CENT BIOTECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Page 1; 7pp; Chinese.
                                                                                                          AAA38947 standard; DNA; 1091
                                                                                                                                                                                                                                                                                                                                                                                                       94TW-0106105.
                                                                                                                                                                         23-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 57.3 Matches 224; Conservative
                                                                                                                                                                                                                                                                        Banana bunchy top virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-316145/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      You L,
                                                                                                                                                                                                                                                                                                                                                                     30-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                     30-JUN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to DNA promoter sequences derived from components of Banana Bunchy Top Virus (BBTV). The DNA molecule includes a promoter sequence derived from an untranslated portion of any one BBTV components and is adaptable for promoting transcription of a cloned gene in a plant cell. The promoter, included in a DNA chimeric vector, is useful for the expression of a gene in a plant cell. The inclusion of the polyubiquitin (ubil) intron sequence into BBTV promoter constructs enhances promoter activity. The present sequence represents the DNA sequence of BBTV S21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 gggaagtccgtgtttgccaaatatctcggactcaagcccgactggttctacacatgtggt 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ggaaccagaaaggacgtattgtaccagtacatcgaggacccaaaacgaaatttaatcctc 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  332 ggaaagtcaaccttcgcaagatatctatcattaaaacctggatggggatatatcaacggt 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           392 ggaaagacgtcggatatgatgcacatcataacgatggatcctgataatcattggattatt 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            272 atcgaaggtgttcctgatgatcgaagtatcatctgggtatacggtcccaacggaggcgaa 331
                                                                        846 catgtaattgttatggcaaatgtgttgcctgattattgtaaaatttcagaagatagaata 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 atcggaggacagcggacgatcgcacaatcctctggatatgcggacgaggaggaggagac 60
786 agagttttaataaatacaaaatacgaaccatgtgtgattagaaaagatggacaaaatgtc 845
                                   Promoter; Banana Bunchy Top Virus; BBTV; gene transcription; ubil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 886;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hermann SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.4%; Score 112.4; DB 20; Length 57.9%; Pred. No. 1.4e-27; tive 0; Mismatches 156; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 886 BP; 294 A; 171 C; 199 G; 222 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                          DNA sequence of BBTV S2I and S2L promoter fragments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Becker DK, Dale JL, Dugdale B, Harding RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Banana Bunchy Top Virus promoter constructs
                                                                                                                   358 aaactgtggaatatttaaagtatgtgtcatc 388
                                                                                                                                                    906 aaaataattaattgttgagaaaggaaacttc 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              promoter and S2L promoter fragments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYQU-) UNIV QUEENSLAND TECHNOLOGY
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                                                                                                                                                                                                                                                                                                                                                                                                                 polyubiquitin 1; banana; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98AU-0004423
                                                                                                                                                                                                                                                AAX34687 standard; DNA; 886
                                                                                                                                                                                                                                                                                                                          02-JUL-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Banana bunchy top virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-254706/21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                  AAX34687
                                                                                                                                                                                                               RESULT
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Banana bunchy top virus; BBTV; PCR technique; plant; tissue; banana;
Musa; phloem damage; aphid; nucleic acid detection; circular; cyclic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This represents the nucleotide sequence of a banana bunchy top virus (BBTW) DNA I (clone 7-4-2) circular single stranded (css) DNA. The invention provides nucleic acid sequences associated with BBTW that can be used in a PCR technique for detecting BBTW. The nucleic acid
            241 agggcattcagttcggacaaatacgaacc---ccttagttatcttgggttcgaccatgtg 297
                                                           572 catgiaattgitatggcaaatgigttgcctgattatigtaaaatttcagaagatagaata 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids having banana bunchy top virus component sequences used to design primers for use in polymerase chain reaction detection of the virus
181 gatgtacccaggtgtaatttagagtatttaaattatgccctgttagaatgtgttaagaac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_except= (pos:335.337, aa:Gly)
/transl_except= (pos:518.520, aa:Ser)
380.385
                                                                                                                                                                                                                                                                                               BBTV DNA I clone (7-4-2) nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "ORF-V2 product"
                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 11A-B; 27pp; English.
                                                                                                                                                                                                                             AAV71832 standard; DNA; 1106 BP
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                                                                                                                                              358 aaactgtggaatatttaa 375
                                                                                                                                                                   632 aaaataattaattgttga 649
                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= b
62..922
/*tag= c
/product= "
                                                                                                                                                                                                                                                                            (first entry)
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901..906
                                                                                                                                                                                                                                                                                                                                                            Banana bunchy top virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Soong T, Wu R, You L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-APR-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polyA_signal
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                                                                                                                                                                                                                                                                                                                                                                                               TATA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                        stem_loop
                                                                                                                                                                                                                                                     AAV71832;
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                                                                                                                                                                                                          RESULT
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sequences (AAV71830 to AAV71833) are used as the basis for the construction of PCR primers, to detect BBTV infection. The PCR technique is used for detecting BBTV in plant tissues (preferably banana, especially Musa species). The virus, one of the most important banana species viruses, causes phloem damage and is transmitted by aphids. PCR detection gives accurate, reliable and specific determination of absence
                                                                                                                                                                                                                                                                                  548 attgacgaggaacccgatgatcgaagcatcatctgggtctatggtccttatggtaatgag 607
                                                                                                                                                                                                                                                                                                                    61 gggaagtccgtgtttgccaaatatctcggactcaagcccgactggttctacacatgtggt 120
                                                                                                                                                                                                                                                                                                                                                  608 ggtaaatcaacatatgcgaagtcactaatcaagaaggattggttctacaccaggggtggg 667
                                                                                                                                                                                                                                                                                                                                                                                    121 ggaaccagaaaggacgtattgtaccagtacatcgaggacccaaaacgaaatttaatcctc 180
                                                                                                                                                                                                                                                                                                                                                                                                                   668 aagaaggagaatatcttattctcctatgtggacgaaggatctgacaagcatatagtattt 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                    gatgtacccaggtgtaatttagagtatttaaattatgccctgttagaatgtgttaagaac 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agggcattcagttcggacaaatacgaaccccttagttatcttgggttcgaccatgtgcat 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 788 agggttatagagagtactaaatacaaacccataaagatagttgaattaggtaaaatacat 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 gtactogtatttgccaatgtcctgcctgattatttgaaaatcagcagggacagaataaaa 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          848 gtaatcgtcatggcgaatttcatgcctgacttctgtaaaatctccgaagatcgaataaaa 907
                                                                                                                                                                                                                                                   1 atcggagagccagcggacgatcgcacaatcctctggatatgcggacgagacggaggagagc 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Two circular single-stranded DNAs associated with banana bunchy top
                                                                                                                                                                                                                           0
                                                                                                                                                                                            Length 1106;
                                                                                                                                                                                                                           Indels
                                                                                                                                    Sequence 1106 BP; 335 A; 225 C; 257 G; 289 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Banana bunchy top virus related nucleotide sequence #1.
                                                                                                                                                                                     11.9%; Score 92.6; DB 20; 52.8%; Pred. No. 9.3e-21; tive 0; Mismatches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Banana bunchy top virus; BBTV; detection; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 ctgtggaatatttaaagta 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 908 atcatttattgctgaagaa 926
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                                                                                                     or presence of the virus.
                                                                                                                                                                                                   Best Local Similarity 52.8
Matches 200; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    top virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-316145/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Banana bunchy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUN-1994;
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                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA38946;
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                                                                         associated with banana bunchy top virus (BBTV) and the encoded proteins. Also described is a method of detecting the BBTV virus using the polymerase chain reaction (PCR). The present sequence represents a BBTV related nucleotide sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                  121 ggaaccagaaaggacgtattgtaccagtacatcgaggacccaaaacgaaatttaatcctc 180
                                                                                                                                                                                                                                                                             gggaagtccgtgtttgccaaatatctcggactcaagcccgactggttctacacatgtggt 120
                                                                                                                                                                                                                                                                                                                                                    608 ggtaaatcaacatatgcgaagtcactaatcaagaaggattggttctacaccaggggtggg 667
                                                                                                                                                                                                                                                                                                                                                                                                                668 aagaaggagaatatcttattctcctatgtggacgaaggatctgacaagcatatagtattt 727
                                                                                                                                                                                                                                                                                                                                                                                                                                               181 gatgtacccaggtgtaatttagagtatttaaattatgccctgttagaatgtgttaagaac 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 agggcattcagttcggacaaatacgaacccttagttatcttgggttcgaccatgtgcat 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               848 gtaatcgtcatggcgaatttcatgcctgacttctgtaaaatctccgaagatcgaataaaa 907
                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                           1 atcggagagccagcaggacgatcgcacaatcctctgatatgcggacgaggaggaggagac 60
                                                         The present invention describes two circular single-stranded DNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                              11.7%; Score 91; DB 21; Length 1106; ilarity 52.5%; Pred. No. 3.3e-20; Conservative 0; Mismatches 180; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             promoter; transcription; transgenic plant; legume;
                                                                                                                                                   Sequence 1106 BP; 335 A; 226 C; 256 G; 289 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Subterranean clover stunt virus isolate F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene expression; crop improvement; ss.
virus and detection of the virus -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                            Claim 1; Page 1; 7pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 ctgtggaatatttaaagta 379
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                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                              Matches 199;
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                                                                                                                                                                                                Query Match
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QΩ
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gene expression; crop improvement; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                829 atgtaattgtgtttgcaaatgtactcccagatttgggaaaattaagtgaagatagaataa 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        589 gcaaatctacatttgcaagacatctgtcattgaaagatggttggggttatctgcctggag 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 gaaccagaaaggacgtattgtaccagtacatcgaggacccaaaacgaaatttaatcctcg 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 649 gaaagacacaagatatgatgcatcttgtgactgctgagcctaagaataattgggtatttg 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atgtacccaggtgtaatttagagtatttaaattatgccctgttagaatgtgttaagaaca 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           709 acatacccagagttagttcagagtatgtgaattatggtgtaatagaacaggttaagaata 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 gggcattcagttcggacaaatacgaacc---ccttagttatcttgggttcgaccatgtgc 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      769 gggtaatggtgaatactaagtatgagccatgtgtaatgcgggatgataatcatcctgttc 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    299 atgtactcgtatttgccaatgtcctgcctgattatttgaaaatcagcagggacagaataa 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               529 tagaggaagaaccagattatagaacgataatctgggtgtatggacctgctggtaatgaag 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 ggaagtccgtgtttgccaaatatctcggactcaagcccgactggttctacacatgtggtg 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 teggagaccagegaegategeacaateetetggatatgeggaeggaeggaggagg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Gaps
                                                                                                                                         Circovirus transcription regulatory sequences and related constructs - useful in plants, esp. leguminous plants, for the modulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                       y Match 11.4%; Score 89; DB 17; Length 1017; Local Similarity 53.8%; Pred. No. 1.5e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCSV; promoter; transcription; transgenic plant; legume;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 175; Indels
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1017 BP; 312 A; 160 C; 265 G; 280 T; 0 other;
                                                                  Khan RI, Larkin PJ;
                                                                                Surin BP, Taylor WC, Waterhouse PM;
                      (CSIR ) COMMONWEALTH SCI & IND RES ORG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   359 aactgtggaatatttaaagtatgtg 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               889 aattaattcgttgttgaaaactctg 913
                                                                                                                                                                                                      Claim 4; Page 62; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAT13161 standard; DNA; 1022 BP
                                                                   Keese PK,
                                       (AUSU ) UNIV AUSTRALIAN NAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 207; Conservative
                                                                     Chu PWG,
                                                                                                                WPI; 1996-160363/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SCSV segment 2.
                                                                                                                                                                             gene expression
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                                                                                   Marshall JS,
                                                                     Boevink PC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT13161;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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The subterranean clover stunt virus (SCSV) genome has at least 7 distinct ssDNA components, designated segments 1-7 (AAT13160-66), each contg. 1 major open reading frame and a non-coding region. Segment 2 is predicted to be a viral replication-associated protein gene. Genetic constructs useful in the genetic engineering of plants (esp. 16 promoter region, and in some cases also a terminator region, selected from segments 1-7. The transcription regulators facilitate expression of foreign genes in plants and also facilitate control of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     307 gtattigccaatgtcctgcctgattatttgaaaatcagcagggacagaataaaactgtgg 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 tecgigittigecaaatateteggaeteaageeegaeiggitetaeaeatgiggiggaaee 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          619 acgagcticgcgaaggaatt---aatcaggtatggatggttttatacagccggagggaag 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   127 agaaaggacgtattgtaccagtacatcgaggacccaaaacgaaatttaatcctcgatgta 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        676 acccaggacgtattatatatgtatgctcaagacccagagaggaatattgcgtttgatgtt 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          736 cccaggtgttcttcggagatgatgaactatcaggcgatggagatgttgaagaacagagtt 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247 ttcagttcggacaaatacgaacccttagttatcttgggttcgaccatgtgcatgtactc 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 gagccagcggacgatcgcacaatcctctggatatgcggacgagacggagaggaggag 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Circovirus transcription regulatory sequences and related constructs - useful in plants, esp. leguminous plants, for the modulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11.3%; Score 88.4; DB 17; Length 1022; 54.3%; Pred. No. 2.4e-19; tive 0; Mismatches 166; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     levels of gene expression in different plant tissue types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1022 BP; 309 A; 183 C; 245 G; 285 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Larkin PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Surin BP, Taylor WC, Waterhouse PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Khan RI,
Subterranean clover stunt virus isolate F.
                                                                                                                                                                                                                                                                                                                                                                                                                       (CSIR ) COMMONWEALTH SCI & IND RES ORG.
                                                  Location/Qualifiers
82..924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 58; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Keese PK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) UNIV AUSTRALIAN NAT.
                                                                                                                                                                                                                                                                                    95WO-AU00552.
                                                                                                                                                                                                                                                                                                                                          94AU-0009281.
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                                                                                                                    /*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chu PWG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-160363/16.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Marshall JS,
                                                                                                                                                                                                                                                                                                                                                                        30-AUG-1994;
                                                                                                                                                                            WO9606932-A1
                                                                                                                                                                                                                                                                                       30-AUG-1995;
                                                                                                                                                                                                                                                                                                                                                07-NOV-1994;
                                                                                                                                                                                                                                  07-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Boevink
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (AUSU
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327 tgattatttgaaaatcagcagggacagaataaaactgtggaatatttaaagtatgtgtca 386 

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387 tctaaattacaccaatacccgcccgc 412

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The invention relates to DNA promoter sequences derived from components of Banana Bunchy Top Virus (BBTV). The DNA molecule includes a promoter sequence derived from an untranslated portion of any one BBTV components and is adaptable for promoting transcription of a cloned gene in a plant cell. The promoter, included in a DNA chimeric vector, is useful for the expression of a gene in a plant cell. The inclusion of the polyubiquitin (ubil) intron sequence into BBTV promoter constructs enhances promoter activity. The present sequence represents the DNA sequence of SI promoter fragment derived from BBTV-SI and includes an open reading frame fragment
                                                                                                                                                                                                            DNA sequence of BBTV S1 promoter fragment including an ORF fragment.
                                                                                                                                                                                                                                             Promoter; Banana Bunchy Top Virus; BBTV; gene transcription; ubil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tch 10.4%; Score 81.2; DB 20; Length 593; al Similarity 55.2%; Pred. No. 5.1e-17; 180; Conservative 0; Mismatches 143; Indels 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hermann SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 593 BP; 189 A; 103 C; 133 G; 168 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dale JL, Dugdale B, Harding RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Banana Bunchy Top Virus promoter constructs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and an intergenic region fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Examples; Fig 22; 84pp; English.
                                                                                                               AAX34686 standard; DNA; 593 BP.
                                                                                                                                                                                                                                                                polyubiquitin 1; banana; ss.
                                                                                                                                                                                                                                                                                                                                                                                                 98WO-AU00786
                                                                                                                                                                                                                                                                                                                                                                                                                                98AU-0004423
                                                                                                                                                                                                                                                                                                                                                                                                                                              97AU-0009339
                                                                                                                                                                             02-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                              Banana bunchy top virus.
 367 aatatttaaa 376
                               916 aattgttgaa 925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                             21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                           30-JUN-1998;
                                                                                                                                                                                                                                                                                                                             W09915646-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                              19-SEP-1997;
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                          90 actcaagcccgactggttctacacatgtggtggaaccagaaaggacgtattgtaccagta 149
                                                                         52 aatgaagaaggactggttctacaccagaggtgggaagaagaagaagaacatactgttctctta 111
                                                                                                                        150 cat---cgaggacccaaaacgaaatttaatcctcgatgtacccaggtgtaatttagagta 206
                                                                                                                                                                    112 cgiggacgaaggatcigagaagcatatigtattigataticcicgcigtaaicaggatia 171
                                                                                                                                                                                                                207 tttaaattatgccctgttagaatgtgttaagaacagggcattcagttcggacaaatacga 266
                                                                                                                                                                                                                                                              172 tttaaattatgatgttatagaggcattaaaggatagggtgatagagagtactaaatataa 231
                                                                                                                                                                                                                                                                                                             267 acccettagttatcttgggttcgaccatgtgcatgtactcgtatttgccaatgtcctgcc 326
                                                                                                                                                                                                                                                                                                                                        232 acctattaagttagttgattaattataatatacatgtaattgtcatggctaatttcatgcc 291
3; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         615 atcgaagaattatttgggtttacggcccaaatggaggagaaggaaagacaacgtatgcaa 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 aatatcteggactcaagecegactggttetacacatgtggtggaaecagaaaggaegtat 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               675 aacatctaatgaagacgaagaatgcgttttattctccaggaggaaaatcattggatatat 734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 tgtaccagtacatcgaggacccaaaacgaaatttaatcctcgatgtacccaggtgtaatt 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     735 gtagactgtataattatgaggatat----tgttatatttgatatccctagatgcaaag 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      200 tagagtatttaaattatgccctgttagaatgtgttaagaacagggcattcagttcggaca 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 aatacgaaccccttagttatcttgggttcgaccatgtgcatgtactcgtatttgccaatg 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 atcgcacaatcctctggatatgcggacgagacggaggaggaggaagtccgtgtttgcca 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated Banana bunchy top virus DNA - useful as diagnostic probes and primers and for producing virus-resistant plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.0%; Score 62.8; DB 19; Length 1110;
53.2%; Pred. No. 1.4e-10;
tive 0; Mismatches 152; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1110 BP; 358 A; 197 C; 275 G; 280 T; 0 other;
                                                                                                                                                                                             Banana bunchy top virus component 1 DNA sequence.
                                                                                                                                                                                                                           BBTV; probe; diagnostic primer; component 1; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dale JL, Harding RM, Karan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Column 23-26; 59pp; English.
352 tattatgcactatgacaatcgtacgc 377
                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organisms e.g. to produce virus-reenhancers or termination signals.
                                                                                    AAV24089 standard; DNA; 1110 BP
                                                                                                                                                                                                                                                                                                                                                                     94US-0202186.
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                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                Banana bunchy top virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-321636/28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  24-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                     24-FEB-1994;
                                                                                                                                                         11-AUG-1998
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                                                                                                                                                                                                                                                                                                                                  26-MAY-1998
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                                                                                                                         AAV24089;
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                                                                       AAV24089
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200 tagagtatttaaattatgcctgttagaatgtgttaagaacagggcattcagttcggaca 259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 tgtaccagtacatcgaggacccaaaacgaaatttaatcctcgatgtacccaggtgtaatt 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              205 gtagactgtataattacgaggatat-----tgttatatttgatattccaagatgcaaag 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 aacatetaatgaagacgagaaatgegttttatteteeaggaggaaateattggatatat 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 atoggagaataatttgggtctatggcccaaatggaggagaaaggaaagacaacgtatgcaa 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 atcgcacaatcctctggatatgcggacgagacggaggaggaggaagtccgtgtttgcca 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
            849 aatatgaacccgttttgaagattg---tagaatatgtcgaagtcattgtaatggctaact 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA from intergenic region of banana bunchy top virus DNA component
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Intergenic regions (AAT49399-409) are derived from genomic DNA components 1-6 (see also AAT49386-90) of banana bunchy top virus (BBTV). A large intergenic region (AAT449405) comparises the insert in plasmid pBT1.1NT, a plasmid obtd. by PCR amplification (see also AAT49427-28) of a full-length BBTV1 clone and cloning of rag1-digested PCR product into pBII01.3. BBTV intergenic regions are useful for promotting, enhancing, regulating or modifying transcription of non-BBTV genes in monocotyledon or dicotyledon transgenic plants. The non-BBTV gene is e.g. an insecticide resistance gene, herbicide resistance gene or growth promoting
                                                                                                                                                                                                                 Banana bunchy top vírus DNA intergenic region 1 insert in pBT1.1NT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.6%; Score 59.6; DB 18; Length 982; 52.6%; Pred. No. 1.6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - useful for promoting, enhancing, regulating or modifying transcription of a non-BBTV gene in transgenic plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      Hafner GJ;
                                                                                                                                                                                                                                             BBTV; intergenic region; promoter; transgenic plant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 982 BP; 316 A; 174 C; 249 G; 243 T; 0 other;
                                       320 tootgootgattatttgaaaatcagcagggacagaataaaactg 363
                                                                 906 teetteegaaggaaggaatetttetgaagategaataaagttg 949
                                                                                                                                                                                                                                                                                                                                                                                                                                      Dugdale B,
                                                                                                                                                                                                                                                                                                                                                                                                             (UYQU-) UNIV QUEENSLAND TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                        Beetham PR, Dale JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Fig 12; 80pp; English.
                                                                                                                                         AAT49405 standard; DNA; 982 BP.
                                                                                                                                                                                                                                                                                                                                                           96WO-AU00335.
                                                                                                                                                                                                                                                                                                                                                                                    95AU-0003285.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181; Conservative
                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                            Banana bunchy top virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1997-034368/03.
                                                                                                                                                                                                                                                                                                                                                           31-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                    31-MAY-1995;
                                                                                                                                                                                                                                                                                                         WO9638554-A1
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                                                                                                                                                                                             23-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harding RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Becker DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                     AAT49405;
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This sequence represents a DNA fragment from the component 1 of the Banana bunchy top virus (BBTV). The DNA molecules can be used as diagnostic probes or primers or can be inserted into plants or other organisms e.g. to produce virus-resistant plants or to act as promoters, enhancers or termination signals.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                200 tagagtatttaaattatgcctgttagaatgtgttaagaacagggcattcagttcggaca 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 aatatotoggaotoaagooogaotggttotacaoatgtggtggaaccagaaaggaogtat 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 tgtaccagtacatcgaggacccaaaacgaaatttaatcctcgatgtacccaggtgtaatt 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 atcgcacaatcctctggatatgcggacgaggacgaggaggagaggcgggaagtccgtgtttgcca 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                            260 aatacgaacccttagttatcttgggttcgaccatgtgcatgtactcgtatttgccaatg 319
                                                                                                                 319 aatatgaacccgttttgaagatag---tagaatatgtcgaagtcattgtaatggctaact 375
Isolated Banana bunchy top virus DNA - useful as diagnostic probes and primers and for producing virus-resistant plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1110 BP; 366 A; 191 C; 276 G; 277 T; 0 other;
                                                                                                                                                                                    320 tootgootgattatttgaaaatcagcagggacagaataaaactg 363
                                                                                                                                                                                                                                         376 teetteegaaggaaggaatettttetgaagategaataaagttg 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Banana bunchy top virus component 1 DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BBTV; probe; diagnostic primer; component 1; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Burns TM, Dale JL, Harding RM, Karan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Column 19-22; 59pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                       AAV24086 standard; DNA; 1110 BP
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260 aatacgaacccttagttatcttgggttcgaccatgtgcatgtactcgtatttgccaatg 319
                                                    850 aatatgaacccgttttgaagatag---tagaatatgtcgaagtcattgtaatggctaact 906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated Banana bunchy top virus {\tt DNA} - useful as diagnostic probes and primers and for producing virus-resistant plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents a DNA fragment from the component 1 of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches 154; Indels
                                                                               320 tectgeetgattatttgaaaateageagggaeagaataaaaetg 363
                                                                                                          907 ttcttccgaaggaaggaatctttctgaagatcgaataaagttg 950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1111 BP; 363 A; 192 C; 276 G; 280 T; 0 other;
                                                                                                                                                                                                                                                              Banana bunchy top virus component 1 DNA sequence.
                                                                                                                                                                                                                                                                                        BBTV; probe; diagnostic primer; component 1; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Karan M;
                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UYQU-) UNIV QUEENSLAND TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       enhancers or termination signals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Fig 11; 59pp; English.
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                                                                                                                                                                             AAV24077 standard; DNA; 1111 BP
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                                                                                                                                                                                                                                    (first entry)
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Matches 181; Conservative
                                                                                                                                                                                                                                                                                                                                                               129..989
                                                                                                                                                                                                                                                                                                                     Banana bunchy top virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dale JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-321636/28
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                                                                                                                                                                                                                                    11-AUG-1998
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                                                                                                                                                                                                        AAV24077;
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                                                                                                                                                    RESULT 14
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200 tagagtatttaaattatgccctgttagaatgtgttaagaacagggcattcagttcggaca 259
                                                                                                                 260 aatacgaacccttagttatcttgggttcgaccatgtgcatgtactcgtatttgccaatg 319
                                                                                                                                                                    877 aatatgaacccgttttgaagatag---tagaatatgtcgaagtcattgtaatggctaact 933
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                                                                                                                                                                                                                                                             320 tectgectgattatttgaaaateageagggaeagaataaaaetg 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1111 BP; 363 A; 192 C; 276 G; 280 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Banana bunchy top virus component 1 DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Column 17-18; 59pp; English.
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enhancers or termination signals.
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Best Local Similarity 52.69
Matches 181; Conservative
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                                                                                                                                                                                                                                1 atcggagagccagcggacga......ccccaacctctgctaaccc 781
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Sequence 13, 1
Sequence 1, 1
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Sequence 2,
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Sequence 1
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/pcTUS_COMB.seq:*
                    Compugen Ltd.
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US-08-418-071-5
US-08-718-071-3
US-08-793-634B-6
US-08-793-186-14
US-08-202-186-11
US-08-202-186-12
US-08-202-186-12
US-08-202-186-12
US-08-202-186-16
US-08-202-186-18
US-08-202-186-18
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US-08-202-186-15
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US-08-202-186-17
US-08-118-17
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US-08-289-222E-5
US-09-054-526B-5
US-08-858-207A-6
US-09-351-414-3
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GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                                  383533 seqs, 122816752 residues
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Listing first 45 summaries
                                                                    OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                               Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match 1
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                                                                                                                                                                                                                                                                        Scoring table:
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Sequence 1, A
Sequence 10,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Rohde, Wolfgang
APPLICANT: Recker, Dieter
APPLICANT: Randles, John W.
APPLICANT: Randles, John W.
APPLICANT: Salamini, Francesco
TITLE OF INVENTION: USE OF VIRUS DNA AS A PROMOTER
FILE REFERENCE: 23232.000311
CURRENT APPLICATION NUMBER: US/09/462,975
CURRENT FILING DATE: 2000-05-17
PRIOR PILING DATE: 1998-07-13
PRIOR FILING DATE: 1998-07-13
PRIOR FILING DATE: 1997-07-16
US-08-482-577B-1

US-08-289-222E-2

US-09-218-176-1

US-09-054-526B-2

US-08-666-968C-228

US-08-666-968C-228

US-08-160-741-1

US-08-150-741-1

US-08-150-741-1

US-08-150-741-1

US-08-150-741-1

US-08-150-741-1

US-08-150-741-1

US-08-150-160-3

US-08-160-3

US-08-160-181-3

US-08-160-181-3

US-09-160-181-4

US-09-160-181-4

US-09-160-181-4

US-09-160-181-4
                                                                                                                                                                                   US-09-626-343-4
                                                                                                                                                                                                                     ALIGNMENTS
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                        ; Sequence 1, Application US/09462975
; Patent No. 6303345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence
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Best Local Similarity
 SEQ ID NO 1
LENGTH: 1291
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US-09-462-975-1
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APPLICANT: Wu, Rey-Yuh
APPLICANT: You, Li-Ru
APPLICANT: Scong, Tal-Seng
TITLE OF INVENTION: NUCLECTION SEQUENCE OF TWO CIRCULAR SSDNA
TITLE OF INVENTION: ASSOCIATED WITH BANANA BUNCHY TOP VIRUS AND METHOD FOR DETE
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                                                                                                                                                                                                                                                                    61 gggaagteegtgtttgeeaaatateteggaeteaageeegaetggttetaeacatgtggt 120
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                                                                                                                                                                                                                                                                                                                                                                                                                              671 GGAAAGACGTCGGATATGATGCACATCATAACGATGGATCCTGATAATCATTGGATTATT 730
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                 1 atcggagagccagcggacgatcgcacaatcctctggatatgcggacgagaggaggagac 60
                                                                                                                                                                                                               3;
                                                                                                                                                                         14.6%; Score 114.2; DB 2; Length 1096; 57.5%; Pred. No. 6.6e-30; tive 0; Mismatches 163; Indels 3;
                                desc "BBTV DNA II (clone 2-17)"
                                                                                                    ; ORGANISM: Banana Bunchy Top Virus (BBTV) US-08-418-071-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/418,071
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NAME: Haley Jr., James F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Floppy disk
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                 MOLECULE TYPE: genomic DNA DESCRIPTION: /desc "BBTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             United States
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                                                                                                                                                                                                                   Matches 225; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
TOPOLOGY: circular
                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                       ORIGINAL SOURCE:
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                                                                      ANTI-SENSE: NO
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APPLICANT: You, Li-Ru
APPLICANT: Scong, Tal-Seng
TITLE OF INVENTION: NUCLECTIDE SEQUENCE OF TWO CIRCULAR SSDNA
TITLE OF INVENTION: ASSOCIATED WITH BANANA BUNCHY TOP VIRUS AND METHOD FOR DETECTI
TITLE OF INVENTION: BANANA BUNCHY TOP VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                        1021 tatcgtttacatcttatgaatatcctgcccaggccgaaggcctgggaggtgctacccggc 1080
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                                                                        cgaaggeegggaacaatatgaategagttatgggegggeecacaataaaagatteeattt 540
 1261 tttgcgcgatcggacggctgagttgatctgg 1291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/418,071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-418-071-4
; Sequence 4, Application US/08418071
; Patent No. 5846705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: DCF
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Word Perfect 5.0 CURRENT APPLICATION DATA:
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TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
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FILING DATE: 06-APR
CLASSIFICATION: 435
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STREET: 12
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HYPOTHETICAL:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                      LENGTH:
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APPLICANT: You, Li-Ru
APPLICANT: You, Li-Ru
APPLICANT: Scong, Tai-Seng
TITLE OF INVENTION: NUCLEOTIDE SEQUENCE OF TWO CIRCULAR SSDNA
TITLE OF INVENTION: ASSOCIATED WITH BANANA BUNCHY TOP VIRUS AND METHOD FOR DETECTI
                                                                                                                                                                                                                                                                                                                                      14.4%; Score 112.6; DB 2; Length 1091; 57.3%; Pred. No. 2.4e-29; tive 0; Mismatches 164; Indels 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                            61 gggaagtccgtgtttgccaaatatctcggactcaagcccgactggttctacacatgtggt 120
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DESCRIPTION: /desc "BBTV DNA II (clone 2)"
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                                                                                                                                                                                                                                                                       ORGANISM: Banana Bunchy Top Virus (BBTV)
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1251 Avenue of the Americas
            REFERENCE/DOCKET NUMBER: 2//94
TELECOMIUNICATION INCORMATION:
TELEPHONE: (212) 596-9000
TELEPHONE: (212) 596-9000
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1091 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 3, Application US/08418071
; Patent No. 5846705
; GENERAL INFORMATION:
REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                        Matches 224; Conservative
                                                                                                                                                    single
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                                                                                                                                                                    TOPOLOGY: circular
                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
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                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                   HYPOTHETICAL:
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61 gggaagtccgtgtttgccaaatatctcggactcaagcccgactggttctacacatgtggt 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: genomic DNA
DESCRIPTION: desc= "BBTV DNA I (clone 7-4-2)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Banana Bunchy Top Virus (BBTV)
                                                                                                          APPLICATION NUMBER: US/08/418,071
FILING DATE: 06-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: DCB-1
TELECOMMINICATION INFORMATION:
              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Waterhouse, Peter M.
                                                               SOFTWARE: Word Perfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/4
                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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APPLICANT: BOEVINK, PETRA C.
APPLICANT: SURIN, Brian P.
APPLICANT: Keese, Paul K.
  Floppy disk
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Matches 200; Conservative
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MEDIUM TYPE:
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US-08-793-634B-2
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11.4%; Score 89; DB 4; Length 1017;
Best Local Similarity 53.8%; Pred. No. 4.2e-21;
Matches 207; Conservative 0; Mismatches 175; Indels
          APPLICANT: Khan, Rafigul I.
APPLICANT: Larkin, Philip J.
APPLICANT: Taylor, william C.
APPLICANT: Marchall, Jorry S.
TITLE OF INVENTION: NOVEL PLANT PROMOTERS AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                         ADDRESSEE: Scully, Scott, Murphy & Presser
STREET: 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,634B
FILING DATE: June 9, 1997
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                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORREY/AGENT INFORMATION:
NAME: DiGiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 105
TELECOMMUNICATION INFORMATION:
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TELEFAX: 516-742-4366
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1017 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                 CORRESPONDENCE ADDRESS:
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: New York
RY: U.S.A.
                                                                                                                                         NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-793-634B-6
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307 gtatttgccaatgtcctgcctgattatttgaaaatcagcagggacagaataaaactgtgg 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            247 ttcagttcggacaaatacgaaccccttagttatcttgggttcgaccatgtgcatgtactc 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 gagccagcggacgatcgcacaatcctctggatatgcggacgaggaggaggaggaag 66
                                                                                                                                APPLICANT: Chu, Paul W.G.
APPLICANT: Waterhouse, Peter M.
APPLICANT: Waterhouse, Peter M.
APPLICANT: Larkin, Philip J.
APPLICANT: Taylor, William C.
APPLICANT: Marchall, Jerry S.
APPLICANT: Marchall, Jerry S.
TITLE OF INVENTION: NOVEL PLANT PROMOTERS AND USES
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                      SEE: Scully, Scott, Murphy & Presser: 400 Garden City Plaza Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/793,634B
FILING DATE: June 9, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
; Sequence 2, Application US/08793634B
; Patent No. 6211431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
                                                                  APPLICANT: BOEVINK, PETRA C. APPLICANT: Surin, Brian P. APPLICANT: Keese, Paul K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: June 9, 1997 CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1022 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 201; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                New York
: U.S.A.
                                                  GENERAL INFORMATION:
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Banana Bunchy Top Virus (BBTV)
                                                                                                                                                     ; Sequence 28, Application US/08973068
; Patent No. 6127604
                                                                                                                                                                                                     APPLICANT: Dale, James Langham
APPLICANT: Harding, Robert Maxwell
APPLICANT: Dugdale, Benjamin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/08202186
Patent No. 5756708
GENERAL INFORMATION:
                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                       US-08-973-068-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Ba
US-08-973-068-28
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 28
LENGTH: 982
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80 aatateteggaeteaageeegaetggttetaeaeatgtggtggaaeeagaaaggaegtat 139
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APPLICANT: BURNS, Thomas M.
APPLICANT: DALE, James L.
APPLICANT: HARDING, Robert M.
TITLE OF INVENTION: DNA Sequences of Banana Bunchy Top Virus
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.0%; Score 62.8; DB 1; Length 1110;
53.2%; Pred. No. 6.7e-12;
ive 0; Mismatches 152; Indels 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71611/102 FIKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              PC-DOS/MS-DOS
                                                                                                                                                          Sequence 14, Application US/08202186 Patent No. 5756708 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: JEFFERY, Donald D.
REGISTRATION NUMBER: 19,980
REPERENCE/DOCKET NUMBER: 7161:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                                           IBM PC compatible
                                                                                                                                                                                                                                                                                                                            Foley & Lardner 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-FEB-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                           Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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183; Conservative
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                                                                             916 AATTGTTGAA 925
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                                                                                                                                           US-08-202-186-14
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Best Local S
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849 AAIAIGAACCCGTITIGAAGAIIG---IAGAAIAIGICGAAGICAIIGIAAIGGCIAACI 905
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APPLICANT: Becthan, Petra Ronald
APPLICANT: Hafner, Gregory John
APPLICANT: Hafner, Gregory John
APPLICANT: Becker, Douglas Kenneth
TITLE OF INVENTION: INPERENT ENDING TO BANANA BUNCHY TOP VIRUS
FILE REFERENCE: 09657/00201
CURRENT APPLICATION NUMBER: US/08/973,068
CURRENT FILING DATE: 1998-03-12
EARLIER APPLICATION NUMBER: PCT/AU96/00335
BARLIER FILING DATE: 1966-05-31
NUMBER OF SEQ ID NOS: 61
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: BURNS, Thomas M.
APPLICANT: BALE, James L.
APPLICANT: HARDING, Robert M.
TITLE OF INVENTION: DNA Sequences of Banana Bunchy Top Virus
NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 982;
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                                                                  320 tcctgcctgattatttgaaaatcagcagggacagaataaaactg 363
                                                                                                               906 TCCTTCCGAAGGAATCTTTTCTGAAGATCAATAAAGTTG 949
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ADDRESSEE:
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APPLICANT: KARAN, Mirko
APPLICANT: BURNS, Thomas M.
APPLICANT: DALE, James L.
APPLICANT: HARDING, Robert M.
TITLE OF INVENTION: DNA Sequences of Banana Bunchy Top Virus
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

7.6%; Score 59.6; DB 1; Length 1110;
Best Local Similarity 52.6%; Pred. No. 8.8e-11;
Matches 181; Conservative 0; Mismatches 154; Indels 9;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,186
                                                                                                                                                                                                                                                                                                                                                                             71611/102 FIKE
                                                                                                                                                                                                                                      UMBER: US/08/202,186
24-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/08202186 Patent No. 5756708
                                                                                                                                                                                                                                                                                                                                  NAME: JEFFERY, Donald D.
REGISTRATION NUMBER: 19,980
REFERENCE/DOCKET NUMBER: 7161:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 202 672 5399
TELET. 904136
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                           E: Foley & Lardner 3000 K Street, N.W.
                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1110 base pairs
                                                                    Washington, D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
EDNESS: single
        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: circular
                                                                                                         ZIP: 20007-5109
                                                                                                                                                                                                                                                                        FILING DATE: 24 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                          USA
                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-202-186-11
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                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a
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260 aatacgaaccccttagttatcttgggttcgaccatgtgcatgtactcgtatttgccaatg 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   676 AACATCTAATGAAGACGAGAAATGCGTTTTATTCTCCAGGAGGAAAATCATTGGATATAT 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140 tgtaccagtacatcgaggacccaaaacgaaatttaatcctcgatgtacccaggtgtaatt 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9; Gaps
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APPLICANT: BURNS, Thomas M.
APPLICANT: DALE, James L.
APPLICANT: HARDING, Robert M.
TITLE OF INVENTION: DNA Sequences of Banana Bunchy Top Virus
NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 7.6%; Score 59.6; DB 1; Length 1111; Best Local Similarity 52.6%; Pred. No. 8.8e-11; Matches 181; Conservative 0; Mismatches 154; Indels 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   320 teetgeetgattatttgaaaateageagggaeagaataaaaetg 363
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                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,186
FILING DATE: 24 FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                   71611/102 FIKE
                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-202-186-12; Sequence 12, Application US/08202186; Patent No. 5756708; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: JEFERY, DONAID D.
REGISTRATION NUMBER: 19,980
REFERENCE/DOCKET NUMBER: 7161.
TELEPOMAUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEPHONE: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
Foley & Lardner 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1111 base pairs
TYPE: nucleic acid
                                                 Washington, D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: single
                                                                                                                      COMPUTER READABLE FORM:
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                                                                                               20007-5109
                                                                          USA
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TOPOLOGY:
US-08-202-186-9
                                                                          COUNTRY:
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CORRESPONDENCE ADDRESS:
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                                 COUNTRY:
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APPLICANT: BURNS, Thomas M.
APPLICANT: BALE, James L.
APPLICANT: BALE, James L.
APPLICANT: HARDING, Robert M.
TITLE OF INVENTION: DNA Sequences of Banana Bunchy Top Virus
NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 7.6%; Score 59.6; DB 1; Length 1111;
Best Local Similarity 52.6%; Pred. No. 8.8e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             320 tectgectgattatttgaaaateageagggaeagaataaaaetg 363
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                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                     71611/102 FIKE
                                                                                                                                                                                       US/08/202,186
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                                                                                                                                                                                                                                                            NAME: JEFFERY, Donald D.
REGISTRATION NUMBER: 19,980
REFERENCE/DOCKET NUMBER: 7161.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                     TELEX: 904136
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1111 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
3000 K Street, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3000 K Street, N.W.
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                                                                                                                                                                                                         24-FEB-1994
                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                          CURRENT APPLICATION DATA:
                     Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 181; Conservative
                                                                          COMPUTER READABLE FORM:
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                                                                                                                                                                                   APPLICATION NUMBER:
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                                                        20007-5109
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                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY:
US-08-202-186-12
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                                     COUNTRY:
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80 aatatctcggactcaagcccgactggttctacacatgtggtggaaccagaaaggacgtat 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.6%; Score 59.6; DB 1; Length 1111; 52.6%; Pred. No. 8.8e-11; ative 0; Mismatches 154; Indels 9
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APPLICANT: KARAN, Mirko
APPLICANT: BURNS, Thomas M.
APPLICANT: DALE, James L.
APPLICANT: DALE, James L.
TITLE OF INVENTION, Robert M.
TITLE OF INVENTION, DNA Sequences of Banana Bunchy Top Virus
NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              320 tcctgcctgattatttgaaaatcagcagggacagaataaaactg 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              934 TCCTTCCGAAGGAAGGAATCTTTCTGAAGATCGAATAAAGTTG 977
                                                                                                                COMPUTER: IBM PC COMPGAMS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
COFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                     71611/102 FIKE
                                                                                                                                                                                                                                UMBER: US/08/202,186
24-FEB-1994
                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: JEFPERY, Donald D.
REGISTRATION NUMBER: 19,980
REFERENCE/DOCKET NUMBER: 71611
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEPHONE: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 16, Application US/08202186 Patent No. 5756708
                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 904136
INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1111 base pairs
Washington, D.C.
                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 181; Conservative
                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                  435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: singl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 129.,989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: circular
                                             20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                CLASSIFICATION:
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                          usa
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RESULT 15
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APPLICANT: BURNS, Thomas M.
APPLICANT: DALE, James L.
APPLICANT: HARDING, Robert M.
TITLE OF INTENTION: DNA Sequences of Banana Bunchy Top Virus
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 52.5%; Pred. No. 2e-10;
Matches 180; Conservative 0; Mismatches 154; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     320 toctgootgattatttgaaaatcagcagggacagaataaaact 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           907 TCCTTCCGAAGGAAGGAATCTTTTCTGAAGATCGAATAAAGCT 949
                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OCHEVERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,186
FILING DATE: 24-FEB-1994
                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: JEFFERY, Donald D.
REGISTRATION NUMBER: 19,980
REFERENCE/DOCKET NUMBER: 71611/102 FIKE
TELECOMMULTOATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 18, Application US/08202186
Patent No. 5756708
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 904136
INPORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1103 base pairs
                   3000 K Street, N.W
Foley & Lardner
                                         Washington, D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: circular
US-08-202-186-16
                                                                         20007-5109
                                                                                                                                                                                                                                                 FILING DATE: 24 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
ADDRESSEE:
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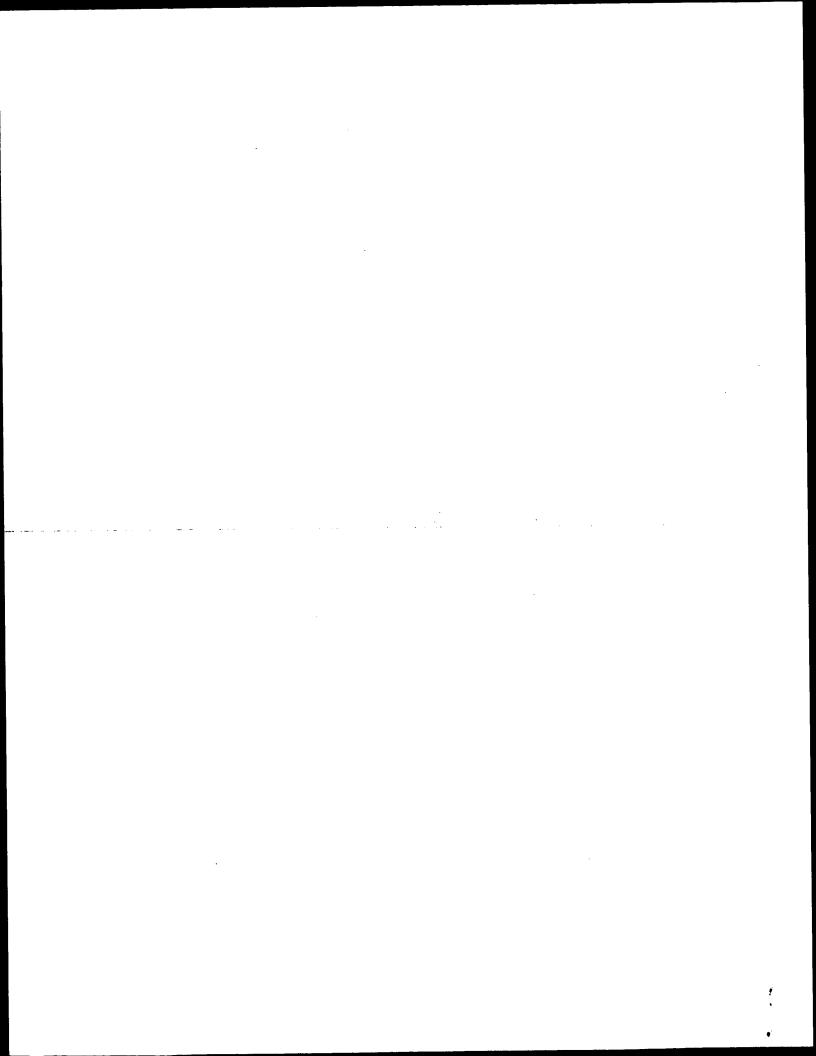
Foley & Lardner

ADDRESSEE:

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260 aatacgaaccccttagttatcttgggttcgaccatgtgcatgtactcgtatttgccaatg 319
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APPLICANT: KRRAN, Mirko
APPLICANT: BURNS, Thomas M.
APPLICANT: DALE, James L.
APPLICANT: HARDING, Robert M.
ITILE OF INVENTION: DNA Sequences of Banana Bunchy Top Virus NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 7.5%; Score 58.6; DB 1; Length 1105; Best Local Similarity 52.5%; Pred. No. 2e-10; Matches 180; Conservative 0; Mismatches 154; Indels 9
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                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,186
FILING DATE: 24-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                            71611/102 FIKE
                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 716
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5399
TELEFAX: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3000 K Street, N.W.
                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: JEFFERY, Donald D.
REGISTRATION NUMBER: 19,980
3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 904136
INFORMATION FOR SEQ ID NO: 18
SEQUENCE CHARACTERISTICS:
LENGTH: 1105 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                           ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: Foley & La
                      Washington, D.C
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                                            COUNTRY:
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7.4%; Score 58; DB 1; Length 1109;
Best Local Similarity 52.3%; Pred. No. 3.2e-10;
Matches 180; Conservative 0; Mismatches 155; Indels
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                                                                                            COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,186
FILING DATE: 24-FEB-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                     71611/102 FIKE
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                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: JEFFERY, Donald D.
REGISTRATION NUMBER: 19,980
REFERENCE/DOCKET NUMBER: 7161.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEPHONE: 202 672 5300
                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 13:
                COUNTRY: USA
ZIP: 2007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 1109 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
US-08-202-186-13
CITY: Washington, D.C.
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June 19, 2002, 14:04:12; Search time 7489.97 Seconds (without alignments) 1407.365 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                     OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                            IDENTITY_NUC Gapon 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                                    Title:
Perfect score:
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                                                                                                                                                                                                                                                                   Sequence:
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                                                                                                                               Run on:
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gb\_gss:\* em\_gss\_hum:\* em\_gss\_inv:\* em\_gss\_pln:\* em\_gss\_vrt:\* 1: em\_estba:\* 2: em\_esthum:\* 3: em\_estin:\* em\_estov:\*
em\_estpl:\*
em\_estro:\* em\_estmu:\* em\_htc:\* gb\_est1:\* gb\_est2:\* gb\_htc:\* 10: 11: 12:

Listing first 45 summaries

EST:\*

Database :

Maximum Match 100%

Post-processing: Minimum Match 0%

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	AV908194 AV908194 AQ121628 HS_3089_A AF034173 AF034173	AL669587 AL669587 AQ615572 HS_5144_B AW818171 CM1-ST027 AL098749 proceeds	AZ444169 1M0239F20 BH137680 ENTPC13TR AQ089903 HS_3001_A AL106734 DrOsophil A1942816 fc67b05.x A108518 Azabidose	AZ401897 1M0168N22 AQ746046 HS_2277_A BH175883 004_P_17- AL612823 T3 end of
SUMMARIES	AV908194 AQ121628 AF034173	AL669587 AQ615572 AW818171 CNS010B7	AZ444169 BH137680 AQ089903 CNS016H0 A1942816 CNSQ000x	AZ401897 AQ746046 BH175883 CNS071RP
DB	9 12	9 12 12	277767	1221
% Query Match Length DB	745 512 2275	706 498 518 787	507 929 318 1101 460 488	345 848 524 524
% Query Match	5.2 5.1 4.9	4 4 4 7 4 4	44444 6.6.6.6.6.6.6.6.6.6.6.6.6.6.6.6.6.	4 4 4 2 . 5 . 5 . 5 . 5 . 5 . 5 . 5 . 5 . 5 .
Score	41 40 38	37.8 36.8 36.8 36.4	36 35.6 35.6 35.4	35.2 35.2 35 35
ult No.	32 1	4597	8 10 11 12 13	14 15 16
Result No.	ου		υυυ	O

/clone="rciad75n04" /clone\_lib="Nori Satoh unpublished cDNA library, young

/organism="Ciona intestinalis" /db\_xref="taxon:7719"

Location/Qualifiers 1. .745

source

2 others

/tissue\_type="whole animal" /dev\_stage="young adult" 121 c 139 g 244 t

239 a

BASE COUNT

0;

Gaps ;

Query Match 5.2%; Score 41; DB 9; Length 745; Best Local Similarity 47.5%; Pred. No. 0.12; Matches 122; Conservative 0; Mismatches 135; Indels

AQ418525 AQ417598 AQ417599 BB633121 BB633121 AG167308 AG167300 AZ397924 AG667528	B1957755 AQ228962 AQ010299 CNSO0DSS AQ807176 AQ807176 AG019820	12         AGL01164         Pan trog1           12         AG131069         AG331069         IMOG056F10           12         AQ488982         IMOC05F10           12         BH135588         BRTDC47TF           12         CNS032C9         BH101848         DROSOPhil           12         CNS032C0         BE779656         GO1464455           12         AQ008775         AQ008775         AQ008775         PCI1-12           10         BG005561         BG006561         QV4-GN014           12         AQ632834         RPC1-11-4         AQ632834         RPC1-11-4           12         AQ728714         AQ632834         RPC1-11-4         AQ632834         RPC1-11-4           12         AQ728714         AQ632834         RPC1-11-4         AQ632834         RPC1-11-4           12         AQ728714         AQ632834         RPC1-11-4         AQ672871         AQ672871           12         AQ481591         AQ673737         CIT-HSP-2         BG787937         BG7873           10         BG787937         BG787937         SRAUMC007         AQ65300         TBNU2187           12         AQ348508         RPCI11-11         AQ348508         RPCI11-11	ALIGNMENTS Satch unpublished cDNA library, young adult Ciona DNA clone rciad75n04 3', mRNA sequence. :16897292 alis. alis. alis.	e; Ciona. ara,Y. and Shin-i,T. a intestinalis 606-8502, Japan col.kyoto-u.ac.jp.
4 6 6 8 8 8 8 8 8 8	90 44 110 41 60	747 747 747 747 747 747 748 748 748 748	94 Nori Sato 94 Nori Sato 94 (G.168) intestinalis intestinalis ota; Metatinalis	onchia; Clonic 1 to 745) Satou,Y., K genes in Cic ed (200) Nori Satoh L of Zoology Fryoto, Kyote Frysto, Frysto, Frysto, Kyote Frysto, Frysto, F
66.00.44 444444	34 4 4 8 8 4 8 4	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	AV908194 AV908194 Nori Satoh intestinalis CDNA cl AV908194 AV908194.1 GI:16897 EST. Ciona intestinalis Ciona intestinalis Ciona intestinalis EVATYOTES, Metazoa;	Phlebobranchia: Cionida 1 (bases 1 to 745) Satoh, N., Satou, Y., Koh Expressed genes in Cion Unpublished (2000) Contact: Nori Satoh Department of Zoology Kyoto University Kyoto Sakyo-ku, Kyoto, Kyoto Tel: 81-75-753-4081 Fax: 81-75-705-1113 Email: satoh@ascidian.z
8 9 0 0 1 2 2 2 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	24 34 34 34 34 33 33 33 33 33 33 33 33 33	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 1 AV908194/C LOCUS LOCUS ACCESSION ACCESSION KEYWORDS SOURCE ORGANISM	REFERENCE STATE TO THE TOTAL T

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AL669587 directional larval cDNA library Clona intestinalis cDNA clone 0502A01 5', mRNA sequence.
                                                                                                                             EST 30-MAR-1998
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Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 706)
                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2275)
Tripodis,N. and Ragoussis,J. Generation of a transcription map in the region immediately centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1529 WKYRKYKKYTSTYYKSWSRWYWYTTYTYWYCWCCTSMKSASCAMMRWMGYMGSRSSRSYW 1588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1589 GYWGSMSGCYGMIKRYYRYSWIGWIKWITWWYMWSMIRWIMIIYTIWWIWRITKIWWWWW 1648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2275 bp mRNA linear EST 30-MAR aF034173 Human mRNA (Tripodis and Ragoussis) Homo sapiens CDNA aF034173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                412 cccacgcgctatcgtttacatcttatgaatatcctgcccaggccgaaggcctgggaggtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Tripodis and Ragoussis)"
99 t. 149 others
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338 aaatcagcagggacagaataaaactgtggaatatttaaagtatgtgtcatct 389
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                     Guys Hospital
7th floor, Guy's Tower, London SE1 9RT, UK
Email: nikos@nki.nl.
                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Tripodis, Nikos
Division of Medical and Molecular Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85; Mismatches
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/db_xref="taxon:9606"
/map="6p21.3"
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619 c 470 g 5
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Ciona intestinalis
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                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
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                                                                                              RESULT
AF034173
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                                                                                                                                                                                                               VERSION
                                                                                                                                                                                                                                                                                                                                                            TITLE
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
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                                            644 TGGTTCAACAAATGCAAGCGCAGATTAAAGCTCAAAGTAAATCAAGTCCCACAGGATCCA 585
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University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
TTEL: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Mahairas GG, Wallace JC, Hood L
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Location/Qualifiers
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Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
IMPORTANT: this sequence may contain errors. The Ciona intestinalis
library from which the clone was isolated may be contaminated with
cDNAs from bacteria or other Eukarya.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                               Directional larval cDNA library originate from Dr.M.Branno, Stazione A.Dohrn, Naples, Italy, and was prepared in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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/note="Vector: pBluescript2SK+" 3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 706;
                    Ciona intestinalis directional larval cDNA library
Unpublished (2002)
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                                                                                                                                                                                                                                                                                                                          /organism="Ciona intestinalis"
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University of Washington
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/clone="050zA01"
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/note="Vector: pBACe3.6; Site_1: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 17-MAY-2000
                                                                                       library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW818171
CM1-ST0277-161299-070-h05 ST0277 Homo sapiens cDNA, mRNA sequence.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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          Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           331 GAAGTCAAATTGTCCCTGTTTGCAGATGACATGATTGTTTAGAAATCCCCATCGAC 390
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                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
/clone="Plate=720 Col=3 Row=D"
/clone_lib="RPCI-11 Human Male BAC Library"
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                           High quality sequence stop: 498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="male"
Tel: (206) 616-3618
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Contact: Robert B. Weiss
University of Utah
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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1 (bases 1 to 507)
2 (bases 1 to 507)
2 (bases 1 to 507)
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1M0239F20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0239F20 F, DNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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/clone="UUGC1M0239F20"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
                                                                                   Length 787;
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                                                                                   Query Match
Best Local Similarity 3.0%; Pred. No. 3.6;
Matches 10; Conservative 109; Mismatches 215;
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Insert Length: 10000 Std Erro:
Plate: 0239 row: F column: 20
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Fax: 801 585 7177
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- Web: www.genoscope.cns.fr)

- Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="Adult"
/note="Organ: stomach; Vector: puc18; Site_1: SmaI;
/note="Organ: stomach; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196.716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSS 26-JUL-1999
Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=CM1.ST0277-161 2.99-070-h05&t3=1999-12-16&t4=1) Seq primer: puc IB forward High quality sequence stort: 76 High quality sequence stort: 76 High quality sequence store: 183.
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Drosophila melanogaster genome survey sequence T7-end of BAC
BACN03M07 of DrosbAC library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 aggacccaaaacgaaatttaatcctcgatgtacccaggtgtaatttagagtatttaaatt 214
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/plasmid="pBeloBAC11"
/db_xref="Laxon:7227"
/clone_lib="DrosBAC"
/clone="BACN03M07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               215 atgccctgttagaatgtgttaagaacagggcattca 250
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                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="ST0277"
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VERSION
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(http://www.jax.org/resources/documents/dnares/). The DNA was bytacoynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of PWD42 (gil4732114)[pb]AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to chemically-competent E. coli XLIO-Gold (Stratagene) cells and.selected for ampicillin resistance."
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Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BH137680 929 bp DNA linear GSS 07-AUG-200
ENTPC137R Entamoeba histolytica Sheared DNA Entamoeba histolytica
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/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 929)
Loftus, B., Wang, Z., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI: MSS sheared DNA library (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          294 tgtgcatgtactcgtatttgccaatgtcctgcctgattatttgaaaatcagcagggacag 353
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Best Local Similarity 58.3%; Pred No. 3.8; Local Similarity 58.3%; Pred No. 3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354 aataaaactgtggaatatttaaagtatgtgtcatctaaattacaccaa 401
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
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                                                                               Laboratory Mouse DNA Resource
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High quality sequence start: 17
High quality sequence stop: 683.
Location/Qualifiers
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BH137680
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Entamoeba histolytica
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Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond, Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.) The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing, A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
ammanla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 318)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         215 atgccctgttagaatgtgttaagaacagggcattcagttcggacaaatacgaaccctta 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           546 ACAAAATTATTATGGACCTACAAGAGTAGAAGGATATTGGAAATATGATTCACCTGAACT 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                666 ATGCCAAGATATAAAAGTAATTATATGATAATTCAAGTACTCATTTACAACAACAAGT 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  606 CTATTATCCAGGTGGAGCATTTCAAATTAATAGTATTAAAAGCTATGACATTACAAGA 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        335 tgaaaatcagcagggacagaataaaactgtggaatatttaaagtatgtgtcatctaaatt 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence-tagged connectors: A sequence approach to mapping and
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Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                         4.6%; Score 36; DB 12; Length 929;
49.5%; Pred. No. 5.2;
Live 0; Mismatches 95; Indels
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University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95; Indels
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/db_xref="taxon:9606"
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Email: jwallace@u.washington.edu
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 49.53
Matches 93; Conservative
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Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               486 TCAACCAT 479
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Location/Qualifiers
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/clone="IMAGE:3726417"
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Seq primer: T7 ET from Amersham
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- Web : www.genoscope.cns.fr)

- Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billand at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACN16B20 of DrosBAC library from Drosophila melanogaster (fruit
    /clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex-"male"
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                                                   /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
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                                                                                                                                                                                                                                                                                                   212 GTTCTGGCCAGGCCAATCAGGCAGGAGGAAATAAAGGGTATTTAATTAGGAAGAGG 153
                                                                                                                                                                                                                                                                                                                                           292 catgtgcatgtactcgtatttgccaatgtcctgcctgattatttgaaaatcagcagggac 351
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/plasmid="pBeloBAC11"
                                                                                                                                                                               Score 35.6; DB 12;
Pred. No. 4.1;
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/clone_lib="DrosBAC"
/clone="BACN16B20"
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sites of the pSPORT1 vector (BRL). Library was constructed by Matthew Clark (Lehrach lab; ICRF, London and Max Planck Institut fuer Molekulare Genetik, Berlin). CDNAS for EST analysis were selected following oligonucleotide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint
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Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S.L., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, S., Hillier, L., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
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/note="Vector: pSPORT1; Site_1: Not1; Site_2: Sal1; lst
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726 DGGGCGAACAGYKTADTGATATGRKAKRSGAARGGWKTGRTGTRRTARTATWGGDRKAGW 785
                                                                             320 tcctgcctgattatttgaaaatcagcagggacagaataaaaactgtggaatatttaaagta 379
                                                                                                                            and Wilson,R.
WashU Zebrafish EST Project 1998
Unpublished (1998)
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tal: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   460 bp mRNA linear EST 07-J
fc67b05.x1 zebrafish WashU MPIMG EST Danio rerio cDNA clone
MAMGE:3726417 3', mRNA sequence.
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409 ccgcccacgcctatcgtttacatcttatgaatatcctgcccaggccga 457

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207 ITGTGTGACACTCTACATGTATTGAATTGTTTCCAATTTACTTAACTTAAGAAAATGAGT 266

DP OY DP

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single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brasslcaceae; Arabidopsis.
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana genome survey sequence SP6 end of BAC F10F11 of IGF library from strain Columbia of Arabidopsis thaliana,
data were used to computationally cluster cDNAs, and a
                                                                                                                                                                                                                                                                  205 tatttaaattatgccctgttagaatgtgttaagaacagggcattcagttcggacaaatac 264
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4.5%; Score 35.4; DB 9; Length 460;
Best Local Similarity 50.9%; Pred. No. 5.7;
Matches 84; Conservative 0; Mismatches 81; Indels (
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Similarity 47.2%; Pred. No. 5.9;
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/clone_lib="IGF"
/clone="F10F11"
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Location/Qualifiers
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(http://www.jax.org/resources/documents/doares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gill772114) fpl.ARL29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for amplicillin resistance."
                                                                                                                                                                     linear GSS 03-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                    1M0168N22R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0168N22 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Mouse 10kb plasmid UUGClM library"
DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: CACACAGGAAACAGCTATGACC
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University of Utah Genome Center
University of Utah
                                                                                                                                                                  345 bp
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/clone="UUGC1M0168N22"
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                                                                                                                                                                                                                                                                       AZ401897.1 GI:10516971
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasmid inserts
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Mammalia: Eutheria: Primates: Catarrhini: Hominidae: Homo.
I (bases: 1 to 84).
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                 AQ746046

HS_2277_A2_F11_T7C CIT Approved Human Genomic Sperm Library D Homo Sapiens genomic clone Plate=2277 Col=22 Row=K, DNA sequence.
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High Throughput Sequencing Center
University of Washington
University of Mashington
101 Queen Anne Avenue North, Seattle, WA 98109, USA
10260 616-3618
Fax: (206) 616-3888
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2277 row: K column: 22
Seq primer: T7
Seq primer: T7
Class: BAC ends
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/db_xref="taxon:9606"
/clone="Plate=2277 Col=22 Row=K"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    232 gitaagaacagggcaitcagitcggacaatacgaacccitagitaictigggitcgac 291
                                                                                                                                                                              0; Gaps
                                                                                          198 tttagagtatttaaattatgccctgttagaatgtgttaagaacagggcattcagttcgga 257
                                                                                                                                  330 TITGAAGAGCITAAAATGGGACGCCTCTGAATGAGGTTATAATATGGTATTACGTCATGA 271
                                                   0; Gaps
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Query Match
Best Local Similarity 55.8%; Pred. No. 5.7;
Matches 67; Conservative 0; Mismatches 53; Indels 0,
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Search completed: June 19, 2002, 14:04:20 Job time: 7518 sec

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Sequence:

Minimum DB Maximum DB

Database

Searched:

M29963 Coconut fol AJ132187 faba bean AJ005966 faba bean U12586 Banana bunc U12587 Banana bunc

AR172770 Sequence

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1 (bases 1 to 1291)
Rohde,W., Becker,D., Randles,J.W., Hehn,A. and Salamini,F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of a virus DNA as promoter
Patent: US 6303345-A 1 16-OCT-2001;
Location/Qualifiers
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Sequence 1 from patent US 6303345.
AR172770 GI:17912261
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FBE132185
                                         NYV5966
BBU12586
BBU12587
AR063451
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AR063453
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AC084298
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AB009047
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AR145398
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AC087476
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                                                                                                                                                                        1 ttagagtatttaaattatgc.......seccaacetetgetaacee 583
                                                                                                                                                                                                                                                                        3595312
          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                           1797656 segs, 10463268293 residues
                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                             US-09-462-955B-1_COPY_409_99
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Perfect score:
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PAT 17-DEC-2001

linear

DNA

84.6%; Score 493; DB 6; Length 1291; 100.0%; Pred. No. 1.6e-134;

Query Match Best Local Similarity

Description

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Score Match Length DB

No. Result

AC05839 Homo sapi AC064832 Homo sapi AC066142 Homo sapi AC024006 Homo sapi AL139214 Human bNA

AR143398 Sequence U16735 Subterranea AJ132185 Edab bean Y14168 Ageratum co AJ238493 Nanovirus AJ005964 faba bean AC02235 Homo sapi AF429315 Homo sapi AF429315 Homo sapi AF188545 Pinus tae AB009047 Milk vetc AC002379 Human BAC

Polymixia Human DNA

AJ005968 1 AP002927 Pc AL442127 AC005176 AC087476

Homo sapi

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AC090536 AC016388

AC026019 AC092899

AC013645

AF216222 Banana bu AB000920 Milk vetc AB000922 Milk vetc

AR063453 Sequence AR063452 Sequence L32167 Banana bunc

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AR063451 Sequence L32166 Banana bur

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/translation="WIGFTWSRPVVPTNRIETTVRRNGCFSSTESRLVLESKGHDWPN DLLRNLANDSAWKTQADTEDALYTELRWNGQDGPLKIRSHFHITIGSLKCCLRSESQRT DALSSGYADETEETGSPCLPNISDSSPTGSTHVVEPERTYCTSTSRTQNEI" complement (422. .568) /note="ORF 6"
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323 9 300 t
                                                                                                                                                                                                                   /translation="MEMGTDFQRPILSIPPKLRVQRIFGIRLGLPGGVHQVPQQIVGP
IVAF"
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                                                                                                                                                                                                                                                                                                                                              _rranslation="MRTRRRREVRVCQISRTQARLVLHMWWNQKGRIVPVHRGPKTK
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                                                                                                                                                                                              /protein_id="AAA42896.1"
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YLKISRDRIKLWNI"
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/db_xref="GI:323307"
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TRPCWKRERLAQRRABEDDELRLEDSGGTRRCVVHGASVERFRAAAENPFFFYHWQ
LEVLSAIGEPADDRIIMICGROGGDGKSVFAKYLGIKPDRFYTGGGRKRDVLYQYIE
DPKRNLILDVPRCNIEXLNYALLECVKNRAFSSDKYEDLSYLGFDHVHVLVFANVLPD
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Rohde, W., Randlas, J.W., Langridge, P. and Hanold, D.
Nucleotide sequence of a circular single-stranded DNA associated
with cocont foliar decay virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    circular; complete genome.
Coconnt foliar decay virus DNA, clones NMORG, pORG, and
Coconnt foliar decay virus
Viruses; ssDNA viruses; Nanovirus.
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Location/Qualifiers
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/note="ORF 1"
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circular VRL 16-SEP-2000
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EPNDRIIIWYYGPNGNEGKSQFGKFLGLKKDYLYLPGGKTQDMTYMLAKNPRANVYMD
IPRCNSEYLNYQFMELIKNRTIFSYKYEPVGCIINNKIHVIVLANVLPDYEKISQDRI
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QLKKKAKMNTVKNIIGGNPHLEKMKGSIEEASAYAQKEESRVAGPWSYGELLKKGSHK
                                                                                                                                                                                                                                                                                                                                                                                                                          Katulli., Timchenko,T., Gronenborn,B. and Vetten,H.J. rinachenko,T., Gronenborn,B. and Vetten,H.J. rom distinct circular ssDNA components, four of which encode putative replication-associated proteins, are associated with the faba bean necrotic yellows virus genome J. Gen. Virol. 79 (Pt 12), 3101-3109 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A single rep protein initiates replication of multiple genome components of faba bean necrotic yellows virus, a single-stranded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (09-JAN-1999) Katul L., Inst. f. Pflanzenvirologie, Mikrobiol., u. biol. Sicherheit, Biologische Bundesanstalt f. Laru. Forstwirtschaft, Messeweg 11 -12, 38104 Braunschweig, GERMANY
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Timchenko,I., de Kouchkovsky,F., Katul,L., David,C., Vetten,H.J.
and Gronenborn,B.
faba bean necrotic yellows virus C9-Eg gene, isolate Egyptian
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J. Virol. 73 (12), 10173-10182 (1999)
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/db_xref="taxon:59817"
/lab_host="Vicia faba"
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1 (bases 1 to 1007)
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                                                                                                                                                                                                                                                                                                     AJ132187.1 GI:4995171
C9-Eg gene; rep protein.
faba bean necrotic yellows virus.
faba bean necrotic yellows virus
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/protein_id="CAB44027.1"
/db_xref="GI:4995172"
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73. 918
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/gene="C9-Eg"
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Katul, L.
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QLKKKAKMNTVKNIIGGNPHLEKMKGSIEEASAYAQKEESRVAGPWSYGELLKKGSHK
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/function="putative replication associated (rep) protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ten distinct circular ssDNA components, four of which encode putative replication associated proteins, are associated with the faba bean necrotic yellows virus genome
J. Gen. Virol. 79 (Pt 12), 3101-3109 (1998)
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                                                                                                                                                                      64 tacgaaccccttagttatcttgggttcgaccatgtgcatgtactcgtatttgccaatgtc 123
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                                                                                                                                                                                                   805 TATGAACCAGTTGGATGTATATAAATAATAAAAATACATGTAATTGTATTAGCTAATGTA 864
                                                     Gaps
                                                                                     4 gagtatttaaattatgccctgttagaatgtgttaagaacagggcattcagttcggacaaa 63
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    11.7%; Score 68.4; DB 14; Length 1007; 62.1%; Pred. No. 3.7e-09; ive 0; Mismatches 66; Indels 0;
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60.9%; Pred. No. 3.2e-08;
tive 0; Mismatches 68;
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1 (bases 1 to 1004)
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/protein_id="CAA06789.1"
/db_xref="GI:3550533"
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Query Match 11.7%
Best Local Similarity 62.1%
Matches 108; Conservative
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73. .918
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GSNRRKLSEMYSRSPERMRIEQPEIYHRYTSVKKLKKFKEEFVHPCLDRPWQIQLTEA
IDEEPDDRTIFWYYGPNGNEGKSTYAKSLMKKDWFYTRGGKKENILFSYVDEGSEKHI
VFDIPRCNQDYLNYDVIEALKDRVIESTKYKPIKLVELNNIHVIVMANFMPEFCKISE
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                                                                                                                                                                                                                                                                                                                  BBU12586 1111 bp DNA circular VRL 01-FEB-1995 Banana bunchy top virus DNA III ORF V1 and ORF C1 genes, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleotide sequences of DNA III and DNA IV associated with banana bunchy top virus and their relation to other closely related virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (25-JUL-1994) Rey-Yuh Wu, Agricultural Biotechnology Division, Development Center for Biotechnology, 81 Chang Hsing Street, Taipei, 10671, Taiwan, ROC Location/Qualifiers
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                                       745 GAATATITAAATTACCAATITATGGAATTAATTAAAAATAGAACCATATATAGTTATAAA 804
                                                                                    64 tacgaacccttagttatcttgggttcgaccatgtgcatgtactcgtatttgccaatgtc 123
                                                                                                                            805 TATGAACCAGTIGGAIGTATTATAAATAATAATACATGTAATTGTATTAGCTAATGTA 864
4 gagtatttaaattatgccctgttagaatgtgttaagaacagggcattcagttcggacaaa 63
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                                                                                                                                                                        124 ctgcctgattatttgaaaatcagcagggacagaataaaactgtggaatatttaa 177
                                                                                                                                                                                                            865 TIGCCIGATIAIGAAAAATIAGICAGGATAGAATTAAAATAATITATIGITAA 918
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/db_xref="taxon:12585"
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/protein_id="AAA61876.1"
/db_xref="G1:642392"
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/db_xref="GI:642391"
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Banana bunchy top virus
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Wu, R.-Y.
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U12586.1 GI:642390
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Matches 109; Conserv
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/translation="MSSFKWCFTLNYSSAABREDFLALLKEEELNYAVGDEVAPSSG
OKHLOGYLSIKKSIKLGGLKKKYSSRAHWERARGSDEDNAKYCKSKFLILELGFPASO
OKHLOGYLSIKKSIKLIGGLKKKYSSRAHWERARGSDEDNAKYCKSKFLILELGFPASO
OKHLOGYLSIKKSIKLIGGLIKKYSSRAHWERARGSDEDNAKT
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                                                                                                                                                                                                                                                                              BBU12587 1127 bp DNA circular VRL 01-FEB-1995
Banana bunchy top virus DNA IV ORF VI and ORF CI genes, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleotide sequences of DNA III and DNA IV associated with banana bunchy top virus and their relation to other closely related virus
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Submitted (25-JUL-1994) Rey-Yuh Wu, Agricultural Biotechnology
Division, Development Center for Biotechnology, 81 Chang Hsing
Street, Talpei, 10671, Talwan, ROC
Location/Qualifiers
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64 tacgaacccttagttatcttgggttcgaccatgtgcatgtactcgtatttgccaatgtc 123
                                     820 TATAAACCTATTAAGTTAGTTGAATTGAATATATACATGTAATTGTAATGGCTAATTTC 879
                                                                          124 ctgcctgattatttgaaaatcagcagggacagaataaaactgtggaatatttaaagtatg 183
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1 (bases 1 to 1127)
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/db_xref="G1:642395"
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/db_xref="G1:642394"
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/note="ORF C1"
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Wu, R.-Y.
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U12587.1 GI:642393
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Matches 111; Conserv
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Banana bunchy top virus component 2.
                                                                                                           /protein_id="AAA51422.1"
/db_xref="G1:520787"
                                                                                                                                                                                                                                                                                              /protein_id="AAA51423.1"
/db_xref="GI:520788"
                                                                                                                                                                                                                      complement(280. .426)
/gene="C3"
                                                                                                                                                                                                                                                                                                                                                    complement(636. .779)
/gene="C1"
                                                                                                                                                                                                                                                                                                                                                                               complement(636. .779)
/gene="C1"
                                                                                                                                                                                                                                                      complement(280. .426)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(760. .912)
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/gene="C2"
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/gene="V1"
62. ^~-
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9. .37
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Banana bunchy top virus (BBTV DNA I) V1 and C1-C3 genes, complete
                                                                                                                                                                                                                                                                                                                            1 (bases I to 1106)
Mu.R.-Y., You,L.-R. and Soong,T.-S.
Nucleotide sequence of two circular SSDNA associated with banana
bunchy top virus and method for detection of banana bunchy top
64 tacgaaccccttagttatcttgggttcgaccatgtgcatgtactcgtatttgccaatgtc 123
              124 ctgcctgattatttgaaaatcagcagggacagaataaaaactgtggaatatttaaagtatg 183
                                                                         749 GATTATTIAAATTATGATGTAATAGAGGCATTAAAGGATAGGGTTATAGAGAGTACTAAA 808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 tacgaaccccttagttatcttgggttcgaccatgtgcatgtactcgtatttgccaatgtc 123
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1 (bases 1 to 1106)

Wu,R.-Y., You,L.-R. and Soong,T.-S.

Nucleotide sequences of two circular single-stranded DNAs associated with banana bunchy top virus
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/db_xref="taxon:12585"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 58; DB 6;
Pred. No. 4.3e-06;
                                                                                                                                                                                                                     DNA
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225 c 257 g
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Banana bunchy top virus DNA.
Banana bunchy top virus
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Best Local Similarity 57.9%;
Matches 103; Conservative
                                                                                                              184 tgtcatctaaattacac 200
                                                                                                                                       940 CGCTATGACAATCGTAC 956
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/translation="MSSPSLKWCFTLNYSSAAERENFLSLLKEEDVHYAVVGDEVAPA
TGOKHLOGTLSLKKRIRLGGLKKKYGSRAHWEIARGTDEENKYCSKETLILELGFPV
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TGOKHLOGTLSLKRSIRLGGLKKYGSRAHWEIARGTDEENCKTCSKETLILELGFPV
EALDEEPDDRSIIWYSGPYGRESKSTYTAKSLIKKDMFTTRGKKENILFSYVDGSDK
HIVFDIPRCNQDYLNYDVIEALKDRVIESTKYKPIKIVELGKIHVIVMANFMDDFCKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AaA51425.1"
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/translation="MIFIRSSEILQKSGMKFAMTITCILPNSTIFMGLYLVLSITLSF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 otgootgattatttgaaaatcagcagggacagaataaaactgtggaatatttaaagta 181
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9.9%; Score 58; DB 14;
Best Local Similarity 57.9%; Pred. No. 4.3e-06;
Matches 103; Conservative 0; Mismatches 75,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA
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Viruses; ssDNA viruses; Nanovirus.
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/translation="MSSFKWGFTLNYSSAABREDFLALLKEEELNYAVYGDEVAPSSG
QKHLQGYLSIKKSIKLGGLKKKYSSRAHWERARGSDEDARAYCKSFETLILELGFPASO
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IDEEDDDRSIIWYSRPHGNEGKSTYAKSLMKKOWFYTRGKKENILESYVDEGSEKHI
VFDIPRCNQDYLNYDVIEALKDRVIESTKKYPIKLVELINIHVIVMANFMPEFCKISE
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                                                                                  Horser, C.L., Karan, M., Harding, R.M. and Dale, J.L. Additional rep-encoding DNAs associated with banana bunchy top
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                                                                                                                                                                                                                       Submitted (14-DEC-1999) school of Life Sciences, Queensland University of Technology, GPO Box 2434, Brisbane, QLD 4001,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 57.4; DB 14; Length 1109;
Pred. No. 6.5e-06;
0; Mismatches 96; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="replication initiation protein"
/protein_id="AAG44003.1"
/db_xref="G1:12004326"
                                                                                                                                  Arch. Virol. 146 (1), 71-86 (2001)
3 (bases 1 to 1109)
Horser,C.L., Karan,M., Harding,R.M. and Dale,J.L.
Direct Submission
                                                                                                                                                                                                                                                                                                                          /organism="Banana bunchy top virus"
              J. Gen. Virol. 82 (Pt 2), 459-464 (2001)
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AR063453
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                                                                                                                                                                                                                                                                                                                                          /isolate="Taiwan"
/db_xref="taxon:12585"
/note="satellite S1"
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63. .917
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Best Local Similarity 54.5%;
Matches 115; Conservative (
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AF216221
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/protein_id="AAA17783.1"
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7GQKHLQGYLSLKKKMPRRIEEEVWLPCSLGDCQRNRRREFEVLFQRNPNPRIRVSCC
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/translation="MIARSPDRMKIEQPEIFHRYQSVNKLKKFKEEFVHPCLDRPWQI
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1 (bases 1 to 1109)

Horser,C., Harding,R. and Dale,J.
Banana bunchy top nanovirus DNA-1 encodes the 'master' replication
                                                                                                                                                               Direct Submission
Submitted (04-0CT-1993) Yu-Chan Chao, Institute of Molecular
Biology, 120, Sec. 2., Yen-joe-yuan Rd., Nan-Kang, Talpei, Taiwan
115, Republic of China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  767 GATTATITAAATTATGATGTAATAGAGGCATTAAAGGATAGGGTTATAGAGAGTACTAAAA 826
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              Yeh, H. H., Su, H. J. and Chao, Y. Genome characterization and identification of viral-associated dsDNA component of banana bunchy top virus Virology 198, 645-652 (1994)
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                                                                                                                                                                                                                                                                                              /spēcific_host="Musa acumināta Colla"
/db_xref="taxon:12585"
                                                                                                                                                                                                                                                                              /organism="Banana bunchy top virus"
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217 c 253 g 288 t
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Banana bunchy top virus
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                                                                                                                2 (bases 1 to 1095)
Chao,Y.
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          1 (bases 1 to 1091)
Wu.R.-Y., You,L.-R. and Soong,T.-S.
Nucleotide sequence of two circular SSDNA associated with banana
bunchy top virus and method for detection of banana bunchy top
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Wu.R.-Y., You,L.-R. and Soong,T.-S.
Nucleotide sequence of two circular SSDNA associated with banana
bunchy top virus and method for detection of banana bunchy top
                                                                                                                                                                                                                                                               aaatacgaacc---ccttagttatcttgggttcgaccatgtgcatgtactcgtatttgcc 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAATACGAACCATGTGTGATTAGAAAAGATGGACAAAATGTCCATGTAATTGTTATGGCA 868
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Pred. No. 0.00022;
0; Mismatches 78; Indels 3,
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                                                                              Patent: US 5846705-A 5 08-DEC-1998;
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                                                                                                                         /organism="unknown"
224 c 248 g
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1. .1096
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231 c 244 g
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Matches 112; Conservative
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briv2 1096 bp DNA linear VRL 30-OCT-1994 Banana bunchy top virus (BBTV DNA II) V1, V2, Cl and C2 genes, complete cds's.
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SKRKKLLDPRFRESPEELKMDDPSKYRKOLAVESIKOARIUSRWYHEKERGWKLIOH
IEGVPDDRSITWVGPBNGGEGKSTRARLSLKPGWGYINGGKTSDMHIITMDPDNHW
IIDIPRSHSDYLNYGVIEOIKNRVLINTKYEPCVIRKDGONVHVIVMANVLPDYCKIS
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/db_xref="G1:520795"
/translation="MGLRPNKRFINYNDFLMHLMIACSASYRVGSTCFLIACGGSFLS
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                                                                                                                                                                                                  Viruses, ssDNA viruses; Nanovirus.

1 (bases 1 to 1096)

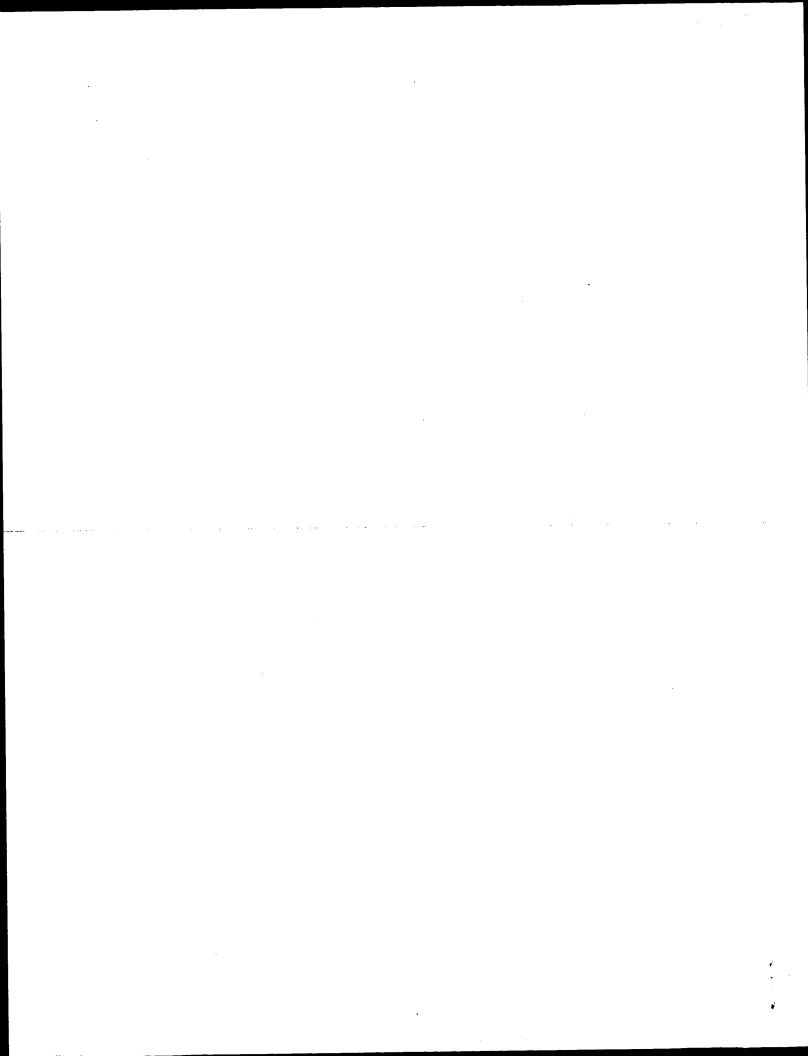
Wu.R.-Y., You,L.-R. and Soong,T.-S.
Nucleotide sequences of two circular single-stranded DNAs associated with banana bunchy top virus
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/db_xref="taxon:12585"
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/db_xref="G1:520792"
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/db_xref="GI:520794"
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Banana bunchy top virus
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/gene="V2"
71. .928
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85. .309
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/function="helicase"
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SKEKRLLEBRERSEPERBOPSKYKRCLAVESINNARKNSBWYHELREMGNKLIOH
IEGVPDDDRSIIWVGPBUGGECKSTFARRLSIKPGWGYINGKTSDMMHITIMDPDNHM
IIDIPRSHSDYLNYGVIEQIKNRVLINTKYEPCVIRKDGQNVHVIVMANVLEDYCKIS
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Banana bunchy top virus satellite S2 replication initiation protein
(ORF V1) gene, complete cds.
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                                                                                                                                                                                                 809 AAATACGAACCATGTGTGATTAGAAAAGATGGACAAAATGTCCATGTAATTGTTATGGCA 868
                                                                                     aaatacgaacc---ccttagttatcttgggttcgaccatgtgcatgtactcgtatttgcc 117
                                                      1 ttagagtatttaaattatgccctgttagaatgtgttaagaacagggcattcagttcggac 60
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                           78; Indels
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/isolate="Taiwan"
           58.0%; Pred. No. 0.00022;
                             Mismatches
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/db_xref="G1:12004328"
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1 (bases 1 to 1095)
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64. .921
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64. .921
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Banana bunchy top virus
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/translation="MPTLQGTFWCFTLNFSGDAPSLSFNERVQYACWOHERVSHDHLO
GYIOWKKRSTLKMMKELLPGAHLEVSRGTPERASDYAAMKEETRVAGFWTYGELLKKGS
GYIOWKKLLDFYRENPEDMELEPPAKARRCRAKIDKEKFIAEFKVEDDEGEWKILEKKIS
KIASPRSILWYGGGGGGGGGGKTSKAKELITRGWRYTRGGKKDDVAYSYVEDPTRHVVFD
IPRDWGEYCNYSLIEMLKDRIIISNKYEPITNCQVXNIHVIWMANFLPDVTKISEDRI
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1 encoding viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (08-FEB-1997) Yoshitaka Sano, Kyoto Institute of Technology, Department of Applied Biology; Matsugasaki, Sakyo-ku, Kyoto 606-8585, Japan (Tel:075-724-7764, Fax:075-724-7764)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 762 AGAATATTGTAATTACAGCTTAATAGAGATGCTTAAGGATAGAATTATTATTAGTAACAA 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 agagtatttaaattatgccctgttagaatgtgttaagaacagggcattcagttcggacaa 62
                                                   61 aaatacgaacc---ccttagttatcttgggttcgaccatgtgcatgtactcgtatttgcc 117
                                                                                                                                                                        118 aatgtootgootgattatttgaaaatoagoaggacagaataaaactgtggaatatttaa 177
                                                                                        On Oct 29, 1998 this sequence version replaced gi:3798651. Sequence updated (30.Sep-1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="viral replication-associated protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    viral replication-associated protein.
milk vetch dwarf virus (lab_host:Pisum sativum) DNA.
milk vetch dwarf virus
                                                                                                                                                                                                                                                                                                                                                                              AB000920 1007 bp DNA circula:
Milk vetch dwarf virus genome segment 1 encoding v:
replication-associated protein, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="milk vetch dwarf virus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; ssDNA viruses; Nanovirus.
1 (bases 1 to 1007)
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/db_xref="GI:3798652"
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- Db Qy
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- 183 gtgt 186
- | || 942 GCGT 945 Qy

Search completed: June 19, 2002, 15:43:34 Job time: 13472 sec



Banana bunchy top
Banana bunchy top
Banana bunchy top
DNA encoding novel

novel novel novel

DNA encoding n
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Banana bunchy top Banana bunchy top

Mouse uromodiling DNA encoding novel DNA encoding novel DNA encoding novel DNA encoding novel DNA encoding novel

top

Banana bunchy

novel

Banana bunchy Banana bunchy

bunchy DNA encoding Banana k Banana k

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Banana bunchy top virus; BBTV, PCR technique; plant; tissue; banana;
Musa; phloem damage; aphid; nucleic acid detection; circular; cyclic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /transl_except= (pos:335.337, aa:G1y)
/transl_except= (pos:518..520, aa:Ser)
380..385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BBTV DNA I clone (7-4-2) nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "ORF-V2 product"
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                                                                                                                                                           AAS73145
AAS74254
AAS77251
AAS68093
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AAZ93966
AAS74278
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AAS81606
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AAV24077
AAV24084
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AAS68231
AAT49405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAV71832 standard; DNA; 1106 BP
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223
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/*tag= a
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/product=
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1105
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1182
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42488
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 polyA_signal
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36.8
35.3
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34.2
34.2
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33.6
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2: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1981.DAT:*
3: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1981.DAT:*
4: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1981.DAT:*
4: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1981.DAT:*
5: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1981.DAT:*
6: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1981.DAT:*
7: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1981.DAT:*
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9: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1981.DAT:*
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15: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1995.DAT:*
16: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1995.DAT:*
16: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1995.DAT:*
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17: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1996.DAT:*
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19: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1996.DAT:*
20: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1996.DAT:*
21: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1999.DAT:*
22: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1999.DAT:*
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                                                                                         (without alignments)
263.504 Million cell updates/sec
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DNA sequence of BB
BBTV DNA II clone
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SCSV segment 6. S
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                                                                                                                                                  1 ttagagtatttaaattatgc......sccccaacctctgctaacccc 583
                                                                          June 19, 2002, 16:51:06 ; Search time 3798.65 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                             1736436 seqs, 858457221 residues
                                                                                                                           US-09-462-955B-1_COPY_409_991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                  OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                             Maximum Match 100%
Listing first 45 summaries
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AAA38947
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AAA38950
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AAT13165
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Maximum DB seq length: 200000000
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Match Length
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(BIOT-) DEV CENT BIOTECHNOLOGY.
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                       Wu R,
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                                                                                                                                                                                                                This represents the nucleotide sequence of a banana bunchy top virus (BBTV) DNA I (clone 7-4-2) circular single stranded (css) DNA. The invention provides nucleic acid sequences associated with BBTV that can be used in a PCR technique for detecting BBTV. The nucleic acid sequences (AAV71830 to AAV71833) are used as the basis for the construction of PCR primers, to detect BBTV infection. The PCR technique is used for detecting BBTV in plant tissues (preferably banana especially Musa species). The virus, one of the most important banana species viruses, causes phloem damage and is transmitted by aphids. PCR detection gives accurate, reliable and specific determination of absence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 tacgaaccettagttatettgggttcgaccatgtgcatgtactcgtatttgccaatgte 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 ctgcctgattatttgaaaatcagcagggacagaataaaactgtggaatatttaaagta 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids having banana bunchy top virus component sequences used to design primers for use in polymerase chain reaction
                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                        Score 58; DB 20; Length 1106; Pred. No. 2.4e-09;
                                                                                                                                                                                                                                                                                                                                                                                                              75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Banana bunchy top virus related nucleotide sequence #1.
                                                                                                                                                                                                                                                                                                                                                       Sequence 1106 BP; 335 A; 225 C; 257 G; 289 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Banana bunchy top virus; BBTV; detection; ds
                                                                                                                                                                                                                                                                                                                                                                                         Query Match 9.9%; Score 58; DB Best Local Similarity 57.9%; Pred. No. 2.4e Matches 103; Conservative 0; Mismatches
                                                                                                                                                                                                Claim 1; Fig 11A-B; 27pp; English.
                                                                        (BIOT-) DEV CENT BIOTECHNOLOGY
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                                                 95US-0418071
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                                                                                                                                                                                                                                                                                                                                   or presence of the virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Banana bunchy top virus.
                                                                                               You L;
                                                                                                                                                                           detection of the virus
                                                                                                                    WPI; 1999-059037/05.
                                                                                                                                P-PSDB; AAW87459.
                                                                                               Wu R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-JUN-1994;
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                             06-APR-1995;
                                                   06-APR-1995;
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       08-DEC-1998
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The present invention describes two circular single-stranded DNAs associated with banana bunchy top virus (BBTV) and the encoded proteins. Also described is a method of detecting the BBTV virus using the polymerase chain reaction (PCR). The present sequence represents a BBTV related nucleotide sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to DNA promoter sequences derived from components of Banana Bunchy Top Virus (BBTV). The DNA molecule includes a promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            749 gattatttaaattatgatgtaatagaggcattaaaggatagggttatagagagtactaaa 808
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         809 tacaaacccataaagatagttgaattaggtaaaatacatgtaatcgtcatggcgaatttc 868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA sequence of BBTV S1 promoter fragment including an ORF fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 gagtatttaaattatgccctgttagaatgtgttaagaacagggcattcagttcggacaaa 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Two circular single-stranded DNAs associated with banana bunchy top virus and detection of the virus \mbox{\ }
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Promoter; Banana Bunchy Top Virus; BBTV; gene transcription; ubil; polyubiquitin 1; banana; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.9%; Score 58; DB 21; Length 1106; 57.9%; Pred. No. 2.4e-09; tive 0; Mismatches 75; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1106 BP; 335 A; 226 C; 256 G; 289 T; 0 other;
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                                                                                                                                                                                       Claim 1; Page 1; 7pp; Chinese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98AU-0004423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Banana bunchy top virus.
You L, Song T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-254706/21
                                                WPI; 2000-316145/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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to detect BBTV infection. The PCR technique is used for detecting BBTV in plant tissues (preferably banana, especially Musa species). The virus, one of the most important banana species viruses, causes phloem damage and is transmitted by aphids. PCR detection gives accurate, reliable and specific determination of absence or presence of the

Sequence 1091 BP; 343 A; 224 C; 248 G; 276 T; 0 other;

virus.

8.56666888

1;

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0;
                    and is adaptable for promoting transcription of a cloned gene in a plant expell. The promoter, included in a DNA chimeric vector, is useful for the expression of a gene in a plant cell. The inclusion of the polyubiquitin 1 (ubil) intron sequence into BBTV promoter constructs enhances promoter fargment derived from BBTV-Sl and includes an open reading frame fragment and an intergenic region fragment.
sequence derived from an untranslated portion of any one BBTV components
                                                                                                                                                                                                                                                                                                                                                      167 gattatttaaattatgatgttatagaggcattaaaggatagggtgatagagagatactaaa 226
                                                                                                                                                                                                                                                                                                                                                                                             tacgaaccccttagttatcttgggttcgaccatgtgcatgtactcgtatttgccaatgtc 123
                                                                                                                                                                                                                                                                                                                                                                                                                              227 tataaaacctattaagttagttgaattgattaatatacatgtaattgtcatggctaatttc 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 ctgcctgattatttgaaaatcagcagggacagaataaaactgtggaatatttaaagtatg 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                 4 gagtatttaaattatgccctgttagaatgtgttaagaacagggcattcagttcggacaaa 63
                                                                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                                         Score 57.4; DB 20; Length 593;
Pred. No. 2.8e-09;
0; Mismatches 96; Indels 0;
                                                                                                                                                                         Sequence 593 BP; 189 A; 103 C; 133 G; 168 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      184 tgtcatctaaattacaccaatacccgcccgc 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           347 aattatattatgcactatgacaatcgtacgc 377
                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                       9.8%;
                                                                                                                                                                                                                                                                            115; Conservative
                                                                                                                                                                                                                                                     Best Local Similarity
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  8886666666666
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Banana bunchy top virus; BBTV; PCR technique; plant; tissue; banana; Musa; phloem damage; aphid; nucleic acid detection; circular; cyclic; ss.
                                                                                                                                                                                                                                                              Nucleic acids having banana bunchy top virus component sequences used to design primers for use in polymerase chain reaction
                                                               BBTV DNA II clone (2) nucleotide sequence.
       AAV71834 standard; DNA; 1091 BP
                                                                                                                                                                                                         (BIOT-) DEV CENT BIOTECHNOLOGY.
                                                                                                                                                                                       95US-0418071.
                                                                                                                                                                     95US-0418071.
                                           10-FEB-1999 (first entry)
                                                                                                               Banana bunchy top virus
                                                                                                                                                                                                                             You L;
                                                                                                                                                                                                                                             WPI; 1999-059037/05.
                                                                                                                                                                                                                            Wu R,
                                                                                                                                                                     06-APR-1995;
                                                                                                                                                                                       06-APR-1995;
                                                                                                                               US5846705-A.
                                                                                                                                                  08-DEC-1998
                           AAV71834;
                                                                                                                                                                                                                            Soong T,
AAV71834
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(BBTV) DNA II (clone 2) and reperesents a subgenomic DNA. The invention provides nucleic acid sequences associated with BBTV that can be used in a PCR technique for detecting BBTV. The nucleic acid sequences (AAV71830 to AAV71833) are used as the basis for the construction of PCR primers,

This represents the nucleotide sequence of a banana bunchy top virus

Disclosure; Fig 12A-C; 27pp; English.

detection of the virus

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associated with banana bunchy top virus (BBTV) and the encoded proteins. Also described is a method of detecting the BBTV virus using the polymerase chain reaction (PCR). The present sequence represents a BBTV related nucleotide sequence from the present invention.
                                                                               61 aaatacgaacc---ccttagttatcttgggttcgaccatgtgcatgtactcgtatttgcc 117
                                                                                                                                     804 aaatacgaaccatgtgtgattagaaaagatggacaaaatgtccatgtaattgttatggca 863
                                                                                                                                                                  aatgtoctgoctgattatttgaaaatcagcagggacagaataaaactgtggaatatttaa 177
                                                                                                                                                                                 1 ttagagtatttaaattatgccctgttagaatgtgttaagaacagggcattcagttcggac 60
                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Two circular single-stranded DNAs associated with banana bunchy top
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes two circular single-stranded DNAs
                               3;
     Length 1091;
                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                           Banana bunchy top virus related nucleotide sequence #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1091 BP; 345 A; 224 C; 247 G; 275 T; 0 other;
9.0%; Score 52.2; DB 20; 58.0%; Pred. No. 2.5e-07;
                             78;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Banana bunchy top virus; BBTV; detection; ds.
                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          virus and detection of the virus
                                                                                                                                                                                                                                                                                                                        AAA38947 standard; DNA; 1091 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94TW-0106105,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94TW-0106105
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                         Matches 112; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Banana bunchy top virus
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                                                                                                                                                                                                                                                    924 gaaaggaaacttc 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Song T;
             Sest Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-1994;
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Query Match
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Claim 2; Columns 17-18; 27pp; English.
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Musa; phloem damage; aphid; nucleic acid detection; circular; cyclic; ss.
                                                                         118 aatgtootgootgattatttgaaaatoagoagggacagaataaaactgtggaatatttaa 177
                                                                                                        61 aaatacgaacc---cettagttatettgggttcgaccatgtgcatgtactcgtatttgcc 117
                                 1 ttagagtatttaaattatgccctgttagaatgtgttaagaacagggcattcagttcggac 60
                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acids having banana bunchy top virus component sequences used to design primers for use in polymerase chain reaction detection of the virus
                   3;
   Score 52.2; DB 21; Length 1091; Pred. No. 2.5e-07;
                    Indels
                                                                                                                                                                                                                                                                                                                                                  transl_except= (pos:215..217, aa:Gly) 33..538
                    78;
                                                                                                                                                                                                                                  BBTV DNA II clone (2-17) nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                            /product= "ORF-V2 product"
                    0; Mismatches
                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                       AAV71833 standard; DNA; 1096 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BIOT-) DEV CENT BIOTECHNOLOGY
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     9.0%;
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1030..1035
/*tag= ge
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8..38
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907..912
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/*tag=
                    Matches 112; Conservative
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                                                                                                                                                                                                                                                                                                                       /*tag=
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                                                                                                                                 178 agtatgtgtcatc 190
                                                                                                                                                924 gaaaggaaacttc 936
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      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAW87460.
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                                                                                                                                                                                                                                                                                                                                                                             polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                           oolyA_signal
                                                                                                                                                                                                                                                                                                                                                             polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                             polyA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                  US5846705-A.
                                                                                                                                                                                                                    10-FEB-1999
                                                                                                                                                                                                                                                                                          Key
TATA_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-DEC-1998
                                                                                                                                                                                                                                                                                                                stem_loop
                                                                                                                                                                                                     AAV71833;
                                                                                                                                                                               AAV71833
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1;
This represents the nucleotide sequence of a banana bunchy top virus (BBTV) DNA II (clone 2-17) circular single stranded (css) DNA. The invention provides nucleic acid sequences associated with BBTV that can be used in a PCR technique for detecting BBTV. The nucleic acid sequences (AAV71830 to AAV71833) are used as the basis for the construction of PCR primers, to detect BBTV infection. The PCR technique is used for detecting BBTV in plant tissues (preferably banana species). The virus, one of the most important banana species viruses, causes phloem damage and is transmitted by aphids. PCR detection gives accurate, reliable and specific determination of absence or presence of the virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 aatgteetgeetgattatttgaaaateageagggaeagaataaaaetgtggaatattaa 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 aaatacgaacc---cettagttatettgggttcgaccatgtgcatgtactcgtatttgcc 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ttagagtatttaaattatgccctgttagaatgtgttaagaacagggcattcagttcggac 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Two circular single-stranded DNAs associated with banana bunchy top
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3;
                                                                                                                                                                                                                                                                                                                                                                                                                    DB 20; Length 1096;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Banana bunchy top virus related nucleotide sequence #5.
                                                                                                                                                                                                                                                                                                                                       Sequence 1096 BP; 347 A; 231 C; 244 G; 274 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78;
                                                                                                                                                                                                                                                                                                                                                                                                            Score 52.2; DB 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Banana bunchy top virus; BBTV; detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                            9.0%; Score ... 58.0%; Pred. No. 2.5e-v. 58.0%; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             virus and detection of the virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA38950 standard; DNA; 1096 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BIOT-) DEV CENT BIOTECHNOLOGY
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Best Local Similarity 58.03
Matches 112; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178 agtatgtgtcatc 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         929 gaaaggaaacttc 941
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Gaps

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The invention relates to DNA promoter sequences derived from components of Banana Bunchy Top Virus (BBTV). The DNA molecule includes a promoter sequence derived from an untranslated portion of any one BBTV components and is adaptable for promoting transcription of a cloned gene in a plant expression of a gene in a plant expression of a gene in a plant cell. The included in a DNA chimeric vector, is useful for the expression of a gene in a plant cell. The inclusion of the polyubiquitin (ubil) intron sequence into BBTV promoter constructs enhances promoter activity. The present sequence represents the DNA sequence of BBTV S21 promoter and S2L promoter fragments.
                                                                                                                                                                                                                                                                 aaatacgaacc.-.ccttagttatcttgggttcgaccatgtgcatgtactcgtatttgcc 117
                                                                                                                                                                                                                                                                                              809 aaatacgaaccatgtgtgattagaaaagatggacaaaatgtccatgtaattgttatggca 868
                                                                                                                                                                                                                                                                                                                                118 aatgteetgeetgattatttgaaaateageagggaeagaataaaaetgggaatatttaa 177
                                                                                                                                                                                                                                                                                                                                                        1 ttagagtatttaaattatgccctgttagaatgtgttaagaacagggcattcagttcggac 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Promoter; Banana Bunchy Top Virus; BBTV; gene transcription; ubil; polyubiquitin 1; banana; ss.
                    Polymerase chain reaction (PCR). The present sequence represents BBTV related nucleotide sequence from the present invention.
Also described is a method of detecting the BBTV virus using the
                                                                                                                                                                3;
                                                                                                                          9.0%; Score 52.2; DB 21; Length 1096; 58.0%; Pred. No. 2.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dugdale B, Harding RM, Hermann SR;
                                                                                                                                                              78; Indels
                                                                     Sequence 1096 BP; 347 A; 231 C; 244 G; 274 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA sequence of BBTV S21 and S2L promoter fragments.
                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Banana Bunchy Top Virus promoter constructs
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                                                                                                                                      Best_Local Similarity 58.0 Matches 112; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                      929 gaaaggaaacttc 941
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-254706/21
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                                                                                                                          Query Match
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   2225×8
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Sequence 886 BP; 294 A; 171 C; 199 G; 222 T; 0 other;

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The subterranean clover stunt virus (SCSV) genome has at least 7 distinct ssDNA components, designated segments 1-7 (AAT13160-66), each congy. 1 major open reading frame and a non-coding region. Segment 6 is predicted to be a viral replication-associated protein gene. Genetic constructs useful in the genetic engineering of plants (esp. legumes) comprise 1 or more heterologous gene(s) operatively linked to a promoter region, and in some cases also a terminator region, selected from segments 1-7. The transcription regulators facilitate expression of foreign genes in plants and also facilitate control of levels of gene expression in different plant tissue types.
                                                                                                                                                                                                 61 aaatacgaacc---cettagttatettgggttegaceatgtgeatgtactegtatttgec 117
                                                                                                                                                530 aaatacgaaccatgtgtgattagaaaagatggacaaaatgtccatgtaattgttatggca 589
                                                                                                                                                                                118 aatgtcctgcctgattatttgaaaatcagcagggacagaataaaactgtggaatatttaa 177
                                   Gaps
                                                         1 ttagagtatttaaattatgccctgttagaatgtgttaagaacagggcattcagttcggac 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Circovirus transcription regulatory sequences and related constructs useful in plants, esp. leguminous plants, for the modulation of
                                                                                    3;
    Length 886;
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 promoter; transcription; transgenic plant; legume;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      han RI, Larkin PJ;
Waterhouse PM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1017 BP; 312 A; 160 C; 265 G; 280 T; 0 other;
 Score 52; DB 20; I
Pred. No. 2.6e-07;
0; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Subterranean clover stunt virus isolate F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Khan RI,
                                                                                                                                                                                                                                                                                                                                                                                                                                gene expression; crop improvement; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Keese PK,
8.98;
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              Best Local Similarity 59.4
Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                   SCSV segment 6.
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                                                                                                                                                                                                                                                                                                                                                     23-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-NOV-1994;
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Marshall JS,
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Query Match
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polypeptide (II) sequences. (I) is useful as hybridisation probes, polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymucleotides are also used in dispinositics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
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                                                                                                                                                                                             786 aagtatgagccatgtgtaatgcgggatgataatcatcctgttcatgtaattgtgtttgca 845
                                                                                                                                                                                                                                    118 aatgiccigocigaitaititgaaaatcagcagggacagaataaaacigiggaataittaa 177
                                                                                                                                                                                                                                                           726 tcagagtatgtgaattatggtgtaatagaacaggttaagaatagggtaatggtgaatact 785
                                                                                                                                                       aaatacgaacc---ccttagttatcttgggttcgaccatgtgcatgtactcgtatttgcc 117
                                                                            1 ttagagtatttaaattatgccctgttagaatgtgttaaagaacagggcattcagttcggac 60
                                           Gaps
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                                       3;
Length 1017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated polynucleotide (I) and
                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding novel human diagnostic protein #6278.
Score 45.6; DB 17;
Pred. No. 4.6e-05;
0; Mismatches 79;
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    7.8%;
56.4%;
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23-AUG-2000; 2000US-0649167
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                             Best Local Similarity 56.4
Matches 106; Conservative
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                           Similarity
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                                                                                                                                                                                                                                                                                                                       178 agtatgtg 185
                                                                                                                                                                                                                                                                                                                                                            906 aaactctg 913
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          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 10
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to rescree normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as
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The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and anino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                             1333 gttctggccagggcaatcaggcaagacaaagaaataaagggtattaagttaggaaaagag 1392
                                                                                                                                                                                                                                                                                                                                                                                                       94 catgtgcatgtactcgtatttgccaatgtcctgcctgattatttgaaaatcagcagggac 153
                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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0
                                                                                                                                                                                                                                                       Score 36.8; DB 23; Length 2885; Pred. No. 0.092;
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                                                                                                                                                                                               Seguence 2885 BP; 1144 A; 623 C; 512 G; 606 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA encoding novel human diagnostic protein #4325.
                                                                                                                                                                                                                                                                                          52;
                                                                                                                                                                                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAS68521 standard; cDNA; 1935 BP.
                                                                                                                                                                                                                                                             6.3%;
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                68; Conservative
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Best Local Similarity
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                imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in tresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques
    food supplement. (II) and its binding partners are useful in medical
                                                                                                                                                                                                                                                                                                                                                                                                                           1411 gttctggccagggcaatcagggcggagaaaagaaataaagggtattcaattaggaaaagag 1470
                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                       34 gttaagaacagggcattcagttcggacaatacgaacccttagttatcttgggttcgac 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1471 gaagtcaaattgtccctgtttgcagatgacatgactgtatatttagaaaacccca 1525
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                                                                                                                                                                                                                                                                                                         Query Match
6.0%; Score 35; DB 23; Length 1935;
Best Local Similarity 56.5%; Pred. No. 0.31;
Matches 65; Conservative 0; Mismatches 50; Indels (
                                                                                                                                                                                                                                                Sequence 1935 BP; 802 A; 414 C; 325 G; 394 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding novel human diagnostic protein #7836.
                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences.
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23-AUG-2000; 2000US-0649167.
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          quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful in medical disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO
restore normal activity of (II) or to treat disease states involving
                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome
                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 catgiggatgiactegiatitgecaaigteeigeeigatiatitgaaaaicagea 148
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                                                                                                                                                                                                                                                                          Sequence 1935 BP; 802 A; 414 C; 325 G; 394 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding novel human diagnostic protein #8903.
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                                                                                                                                                                                                                                                                                                                                                  Pred. No. 0.31;
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Seguence 1103 BP; 355 A; 192 C; 277 G; 279 T; 0 other;

X OS

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considering expressed genes. (I) is useful in gene therapy techniques for identifying expressed genes. (I) is useful in gene therapy techniques for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical ingorages involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Specification, but was obtained in electronic format directly from WIPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a DNA fragment from the component 1 of the Banana bunchy top virus (BBTV). The DNA molecules can be used as diagnostic probes or primers or can be inserted into plants or other organisms e.g. to produce virus-resistant plants or to act as promoters, enhancers or termination signals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           525 GTTCTGGCCAGGGCAATCAGGGCGGAGAAAGAAATAAAGGGTATTCAATTAGGAAAAAGA 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 gitaagaacagggcaitcagitcggacaaatacgaaccccitagitaicitgggitcgac 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated Banana bunchy top virus DNA - useful as diagnostic probes and primers and for producing virus-resistant plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94 catgtgcatgtactcgtatttgccaatgtcctgcctgattatttgaaaatcagca 148
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0
and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 35; DB 23; Length 1935;
Pred. No. 0.31;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1935 BP; 394 A; 325 C; 414 G; 802 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Banana bunchy top virus component 1 DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BBTV; probe; diagnostic primer; component 1; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dale JL, Harding RM, Karan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Column 25-28; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYQU-) UNIV QUEENSLAND TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAV24091 standard; DNA; 1103 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.0%;
56.5%;
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Best Local Similarity 56.55
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Banana bunchy top virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 tacgaacccttagttatcttgggttcgaccatgtgcatgtactcgtatttgccaatgtc 123
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                                                                                                                   64 tacgaaccccttagttatcttgggttcgaccatgtgcatgtactcgtatttgccaatgtc 123
                                                                                                                                              852 tatgaacccgttttgaaaattg---tagaatatgtggaagtcattgtaatggctaacttc 908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
                                                                              Gaps
                                                         4 gagtatttaaattatgccctgttagaatgtgttaagaacagggcattcagttcggacaaa 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - useful as diagnostic probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 gagtatttaaattatgccctgttagaatgtgttaagaacagggcattcagttcggacaaa
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m
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                              3;
5.9%; Score 34.6; DB 19; Length 1103; 55.3%; Pred. No. 0.32; tive 0; Mismatches 69; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and primers and for producing virus-resistant plants
                                                                                                                                                                             124 ctgcctgattatttgaaaatcagcagggacagaataaaact 164
                                                                                                                                                                                                        909 cttccgaaggaaggaatcttttctgaagatcgaataaagct 949
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Column 29-30; 59pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated Banana bunchy top virus DNA
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                                                                                                                                                                                                                                                                                 BP.
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Best Local Similarity 55.39
watches 89; Conservative
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                                    89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              Banana bunchy top virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-321636/28.
                      Best Local Similarity
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         Query Match
                                                                                                                                                                                                                                                        RESULT 15
                                       Matches
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                          383533 seqs, 122816752 residues
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Perfect score:
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Maximum Match 100% Listing first 45 summaries

Issued\_Patents\_NA:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			SUMMARIES	
Result	or COS	Query	Query Match Longth	9	4	
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1	493	84.6	1291	4	US-09-462-975-1	Segmence 1 Appli
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11	32.4		982	٣	US-08-973-068-28	28
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17			1110	Н	US-08-202-186-11	; ; ;
18	30.8	5.3	1111	Н	US-08-202-186-10	
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21	30	5.1	265	4	US-09-054-526B-5	'n
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c 23	30	5.1	2088	4	US-09-351-414-3	
24	30	5.1	2272	_	US-08-482-577B-1	` <del>- `</del>
25	30	5.1	2272	٣	US-08-289-222E-2	7
56	30	5.1	27	4	-09-218-1	,
27	30	5.1	2272	4	US-09-054-526B-2	Sequence 2, Appli

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Gaps 0;

Length 1291;

84.6%; Score 493; DB 4; Length 12 100.0%; Pred. No. 3.5e-165; Live 0; Mismatches 0; Indels

Matches 493; Conservative Query Match Best Local Similarity

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61 aaatacgaaccccttagttatcttgggttcgaccatgtgcatgtactcgtatttgccaat 120  121 gtcctgcctgattatttgaaaatcagcaggacagaataaaactgtggaatatttaaagt 180

Sequence 2, Appli Sequence 228, Appli Sequence 128, Appli Sequence 11, Appli Sequence 10, Appli Sequence 2, Appli Sequence 3, Appli Sequence 1, Appli Sequence 2, Appli		Sequence:/note=synthetic
US-09-280-409-2 US-08-79-634B-2 US-08-68-686C-228 US-08-150-741-1 US-09-150-741-1 US-09-150-741-1 US-08-09-3 US-08-624-581-3 US-08-624-581-3 US-08-624-581-1 US-09-004-838-94 US-08-526-964-1 US-09-011-897-1 US-09-257-770-1 US-09-259-968-2 US-08-599-968-2 US-08-904-284-6	ULT 1  Gquence 1, Application US/09462975  atent No. 6303345  APPLICANT: Rohde, Wolfgang APPLICANT: Rende, Wolfgang APPLICANT: Rendes, John W. APPLICANT: Randles, John W. APPLICANT: Randles, John W. APPLICANT: Randles, John W. APPLICANT: Randles, John W. APPLICANT: Alain APPLICANT: Balamini, Francesco TITLE OF INVENTION: USE OF VIRUS DNA AS A PROMOTER FILE REFERENCE: 2322.00331 CURRENT APPLICATION NUMBER: US/09/462,975 CURRENT PILING DATE: 1998-07-17 PRIOR APPLICATION NUMBER: PCT/EP98/04345 PRIOR APPLICATION NUMBER: PCT/EP98/04345 PRIOR APPLICATION NUMBER: 1977-07-16 NUMBER OF ESQ ID NOS: 7  LENGYARE: FastESQ for Windows Version 4.0  LENGTH: 1291	Artificial
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859 1022 1102 1102 1020 8920 8920 2899 2899 2817 2959 2483 2483 2483 19523 1701 1701	ALL Application US/09462975 330348 Rende, Wolfgang Becker, Dieter Randles, John W. Hehn, Alain Salamini, Francesco VENTION: USE OF VIRUS DI NECE: 2322.000301 FLICATION NUMBER: US/09/44 ING DATE: 1998-07-13 COATION NUMBER: 19730502 GO DATE: 1997-07-16 SEQ ID NOS: 7 FRASESEQ for Windows Vers.	il Sequence Description of construct
NNUNNN44444444444 0.0.0.0.0.0.0.0.0.0.0.0.0.0.	pplication 03345 MAIJON: Rohde, Wolf Rohde, Wolf Becker, Die Randles, Jo Hehn, Alain Salamini, F ENTION: US CE: 23232. CE: 23232. CE: 1993 ATION NUMBE: 1993	ficia ION: ION:
200902020202020202020202020202020202020	NESULT 1 Sequence 1, Application US/0946297 Sequence 1, Application US/0946297 GENERAL INFORMATION: APPLICANT: Becker, Dieter APPLICANT: Becker, Dieter APPLICANT: Becker, John W. APPLICANT: Becker, John W. TITLE OF INVENTION: USE OF VIRUS FILE REFERENCE: 2323.00031 CURRENT APPLICATION UNMBER: US/09, CURRENT FILING DATE: 2000-05-17 PRIOR FILING DATE: 1999-07-16 NUMBER OF SEQ ID NOS: 7 SEQ ID NOS: 7 SEQ ID NOS: 7 LENGTH: 1291	TITE: DNA PREATURE: FEATURE: OTHER INFORMATION: CC 9-462-975-1
20000000000000000000000000000000000000	NULT Application  Application  APPLICATION  APPLICATION  APPLICATION  APPLICATION  APPLICATION  APPLICATION  PRIOR  PRIOR  PRIOR  PRIOR  NUMBER  SOFTWAN  SOFTWAN  SOFTWAN  SOFTWAN  LENGT	TIFE: ORGAN FEATU OTHER OTHER
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Sequence 5, Application US/08418071
Patent No. 5846705
GENERAL INFORMATION:
APPLICANT: Wou, Key-Yuh
APPLICANT: Soong, Tai-Seng
TITLE OF INVENTION: ASSOCIATED WITH BANANA BUNCHY TOP VIRUS AND METHOD FOR DETE
TITLE OF INVENTION: BANANA BUNCHY TOP VIRUS
NUMBER OF SEQUENCES: 18
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                                                                       749 GATTATTTAAATTATGATGTAATAGAGGCATTAAAGGATAGGGTTATAGAGAGTACTAAA 808
                                                                                                              64 tacgaaccecttagttatcttgggttcgaccatgtgcatgtactcgtatttgccaatgtc 123
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                                     4 gagtatttaaattatgccctgttagaatgtgttaagaacagggcattcagttcggacaaa 63
 0; Gaps
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                                                                                                                                                                                                            Length 1091;
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     75; Indels
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58.0%; Pred. No. 1.6e-08;
tive 0; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: subgenomic DNA
DESCRIPTION: /desc "BBTV DNA II (clone 2)"
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Banana Bunchy Top Virus (BBTV)
     0; Mismatches
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1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UMBER: US/08/418,071
06-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 5.0 CURRENT APPLICATION DATA: US/08/418,07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 27,794
REFERENCE/DOCKET NUMBER: DCB-1
TELEPHONE: (212) 596-9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9000
INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 06-APR-1995
CLASSIFICATION: 435
ATORNEY/AGENT INFORMATION:
NAME: HALEY JT., James F.
REGISTRATION NUMBER: 27,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1091 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            United States
       Matches 103; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
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COMPUTER READABLE FORM:
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ADDRESSEE: Fish & Ne
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US-08-418-071-5
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                                                                                                                                                                                                                                                                                         RESULT 3
US-08-418-071-5
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APPLICANT: Wu, Rey-Yuh
APPLICANT: You, Li-Ru
APPLICANT: Soong, Tai-Seng
TITLE OF INVENTION: NUCLECTIED SEQUENCE OF TWO CIRCULAR SSDNA
TITLE OF INVENTION: ASSOCIATED WITH BANANA BUNCHY TOP VIRUS AND METHOD FOR DETECTI
TITLE OF INVENTION: BANANA BUNCHY TOP VIRUS
                                                                                                                                                                                                                                   1099 tgaatcgagttatgggcgggcccacaataaaagattccatttggataagaacgaatctgt 1158
                                                                                                                                                                                  tactttgcttgcagtgcacgcaaccactttccacgtcaccaatccaggtgagtagcttgc 420
                                                                                   301 tgaatcgagttatgggcgggcccacaataaaagattccatttggataagaacgaatctgt 360
           241 aatateetgeeeaggeegaaggeetgggaagtgetaeeeggeegaaggeegggaacaata 300
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Pred. No. 1.4e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1251 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/418,071
FILING DATE: 06-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 5.0
CURRENT APPLICATION DATA:
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TELEPHONE: (212) 596-9000
TELEFRAX: (212) 596-9000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1106 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08418071
Patent No. 5846705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
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ADDRESSEE: Fish & Neave
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US-08-418-071-3
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809 AAATACGAACCATGTGTGATTAGAAAAGATGGACAAAATGTCCATGTAATTGTTATGGCA 868
                                         118 aatgteetgeetgattatttgaaaateageagggaeagaataaaactgtggaatatttaa 177
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APPLICANT: Keese, Paul K.
APPLICANT: Chu, Paul W.G.
APPLICANT: Waterhouse, Peter M.
APPLICANT: Larkin, Philip J.
APPLICANT: Taylor, William C.
APPLICANT: Taylor, William C.
APPLICANT: Taylor, William C.
APPLICANT: Narchall, Jerry S.
TITLE OF INVENTION: NOVEL PLANT PROMOTERS AND USES
NUMBER OF SEQUENCES: 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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56.4%; Pred. No. 3.3e-06;
1ve 0; Mismatches 79;
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June 9, 1997
                                                                                                                                                                                                                                                          Sequence 6, Application US/08793634B Patent No. 6211431 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MC-SOFFWARDEN
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REGISTRATION NUMBER: 31,346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
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                                                                                                                                                                                                                                                                                                                           APPLICANT: Boevink, Petra C.
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LENGTH: 1017 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 56.43
Matches 106; Conservative
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy
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                                                                                                                       178 agtatgtgtcatc 190
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CITY: Garden City
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                            929 GAAAGGAAACTTC 941
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US-08-793-634B-6
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APPLICANT: You, Li-Ru
APPLICANT: Soong, Tal-Seng
TITLE OF INVENTION: NUCLEOTIDE SEQUENCE OF TWO CIRCULAR SSDNA
TITLE OF INVENTION: ASSOCIATED WITH BANANA BUNCHY TOP VIRUS AND METHOD FOR DETECTI
TITLE OF INVENTION: BANANA BUNCHY TOP VIRUS
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                                                                                                  aaatacgaacc---ccttagttatcttgggttcgaccatgtgcatgtactcgtatttgcc 117
                                         804 AAATACGAACCATGTGTGATTAGAAAAGATGGACAAAATGTCCATGTAATTGTTATGGCA 863
                                                                                 118 aatgtcctgcctgattatttgaaaatcagcagggacagaataaaactgtggaatatttaa 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: genomic DNA DESCRIPTION: /desc "BBTV DNA II (clone 2-17)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Banana Bunchy Top Virus (BBTV) US-08-418-071-4
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06-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 5.0 CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                    Sequence 4, Application US/08418071
Patent No. 5846705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27,794
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FILING DATE: 06-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HALEY JT., JAMES F.
REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
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MEDIUM TYPE: Floppy
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APPLICANT: Wu, Rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New York
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APPLICANT: KARAN, Mirko
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                                         APPLICANT:
                                                            APPLICANT:
                                                                                                                                                                STREET:
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64 tacgaaccccttagttatcttgggttcgaccatgtgcatgtactcgtatttgccaatgtc 123
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                                                                                                                                                                                                                                               APPLICANT: KARAN, Mirko
APPLICANT: KARAN, Mirko
APPLICANT: DALE, James L.
APPLICANT: DALE, James L.
APPLICANT: HARDING, Robert M.
TITLE OF INVENTION: Robert M.
CORRESPONDENCE ADDRESS: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5.9%; Score 34.6; DB 1; Length 1103; 55.3%; Pred. No. 0.028; tive 0; Mismatches 69; Indels 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,186
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                                                                                                                                                                                               Sequence 16, Application US/08202186 Patent No. 5756708 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 24-FEB-1994
CLASSIFICATION: 435
ATGNREY, AGENT INFORMATION:
NAME: JEFERY, DORALD D.
REGISTRATION NUMBER: 19,980
REFERENCE/DOCKET NUMBER: 71611
TELEPHONE: 202 672 5399
TELEFAX: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-202-186-18; Sequence 18, Application US/08202186; Patent No. 5756708; Patent INFORMATION:
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INFORMATION FOR SEQ ID NO: 16:
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LENGTH: 1103 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: circular
US-08-202-186-16
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Best Local Similarity
Matches 89; Conserva
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64 tacgaaccccttagttatcttgggttcgaccatgtgcatgtactcgtatttgccaatgtc 123
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Patent No. 5756708
GENERAL INFORMATION:
BAPPLICANT: BURNS, Thomas M.
APPLICANT: BURNS, Thomas L.
APPLICANT: HARDING, Robert M.
TITLE OF INVENTION: DNA Sequences of Banana Bunchy Top Virus
BURNS, Thomas M.
DALE, James L.
HARDING, Robert M.
WENTION: DNA Sequences of Banana Bunchy Top Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 5.9%; Score 34.6; DB 1; Length 1 Best Local Similarity 55.3%; Pred. No. 0.028; Matches 89; Conservative 0; Mismatches 69; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,186
FILING DATE: 24 FEB-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71611/102 FIKE
                                                                                                                                                                                                                       ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: JEFFERY Donald D.
REGISTRATION NUMBER: 19,980
REFERENCE/DOCKET NUMBER: 71611
TELECOMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFRX: 202 672 5309
TELERX: 904136
INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS:
                                                                                                                                                     : 3000 K Street, N.W. Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 3000 K Street, N.W. CITY: Washington, D.C. COUNTRY: USA ZIP: 20007-5109
                                                                                                                                     Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Foley & Lardner
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                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                   TITLE OF INVENTION:
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5.7%; Score 33; DB 1; Length 1104;
         TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1111 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: JEFFERY, Donald D. REGISTRATION NUMBER: 19,980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W. CITY: Washington, D.C.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 24-FEB-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1104 base pairs
TYPE: nucleic acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                               circular
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                                                                                                                                                             ; TOPOLOGY:
US-08-202-186-12
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US-08-202-186-17
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APPLICANT: BURNS, Thomas M.
APPLICANT: DALE, James L.
APPLICANT: HARDING, Robert M.
TITLE OF INVENTYON: DNA Sequences of Banana Bunchy Top Virus
CORRESPONDENCE: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.8%; Score 34; DB 1; Length 1110;
54.9%; Pred. No. 0.047;
tive 0; Mismatches 70; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           908 CTTCCGAAGGAAGGAATCTTTTCTGAAGATCGAATAAAGTTG 949
                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                              71611/102 FIKE
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NI: 435
                                                                                                    US/08/202,186
                                               PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 12, Application US/08202186 Patent No. 5756708
                                                                                                                                                                 NAME: JEFFERY, Donald D.
REGISTRATION NUMBER: 19,980
REFERENCE/DOCKET NUMBER: 7161:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: JEFFERY, Donald D. REGISTRATION NUMBER: 19,980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                               TELEFAX: 202 672 5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W. CITY: Washington, D.C.
                                                                                                APPLICATION NUMBER: US/08
FILING DATE: 24-FEB-1994
                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                          LENGTH: 1110 base pairs
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Matches 89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                   SS: single circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: singl
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                         COMPUTER: IBM PC OPERATING SYSTEM:
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                                                                                                                                   CLASSIFICATION:
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US-08-202-186-14
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64 tacgaacccttagttatcttgggttcgaccatgtgcatgtactcgtatttgccaatgtc 123
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Patent No. 5756708
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BURNO, Thomas M.
APPLICANT: DALE, James L.
APPLICANT: HARDING, Robert M.
TITLE OF INVENTION: DNA Sequences of Banana Bunchy TOP Virus
Query Match 5.8%; Score 34; DB 1; Length 1111; Best Local Similarity 54.9%; Pred. No. 0.047; Matches 89; Conservative 0; Mismatches 70; Indels
                                                                                                                                                                                                                                                                                                                       909 CTTCCGAAGGAATCTTTCTGAAGATCGAATAAAGTTG 950
                                                                                                                                                                                                                                                                                         124 ctgcctgattatttgaaaatcagcagggacagaataaaactg 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,186
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N: 435
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Washington, D.C.

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                                                                                                                                                                                                                     853 TATGAACCCGTTTTGAAATTG----TAGAATATGTGGAAGTCATTGTAATGGCTAACTTC 909
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                                                                                                                      793 GAATATTTAAACTATGGTTTATTAGAAGAATTTAAAAATGGAATTATTCAAAGCGGGAAA 852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 gagtatttaaattatgccctgttagaatgtgttaagaacagggcattcagttcggacaaa 63
                       3; Gaps
                                                                        4 gagtatttaaattatgccctgttagaatgtgttaagaacagggcattcagttcggacaaa 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Hacker, Gregory John
APPLICANT: Becker, Douglas Kenneth
TITLE OF INTENTION: INTERGEBRIC REGIONS OF BANANA BUNCHY TOP VIRUS
FILE REFERENCE: 09657/002001
CURRENT APPLICATION NUMBER: US/08/973,068
CURRENT FILING DATE: 1998-03-12
EARLIER APPLICATION NUMBER: PCT/AU96/00335
EARLIER APPLICATION NUMBER: PCT/AU96/00335
SARLIER APPLICATION NUMBER: PCT/AU96/00335
SOFTWARE: FAILNG DATE: 1996-05-31
NUMBER OF SEQ ID NOS: 61
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APPLICANT: RARAN, Mirko
APPLICANT: BURNS, Thomas M.
APPLICANT: DALE, James L.
APPLICANT: HARDING, Robert M.
TITLE OF INVENTION: DNA Sequences of Banana Bunchy Top Virus
NUMBER OF SEQUENCE: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.6%; Score 32.4; DB 3; Length 982; 54.3%; Pred. No. 0.16; tive 0; Mismatches 71; Indels
                       Indels
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                                                                                                                                                                                                                                                                         124 ctgcctgattatttgaaaatcagcagggacagaataaaact 164
                                                                                                                                                                                                                                                                                                   910 CTTCCGAAGGAAGCTTTTTTTTGAAGATCGAATAAAGCT 950
                    70;
54.7%; Pred. No. 0.11;
                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Banana Bunchy Top Virus (BBTV) US-08-973-068-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 13, Application US/08202186 Patent No. 5756708
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 28, Application US/08973068 Patent No. 6127604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Dale, James Langham
PAPLICANT: Harding, Robert Maxwell
APPLICANT: Dugdale, Benjamin
APPLICANT: Beetham, Peter Ronald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3000 K Street, N.W.
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                       88; Conservative
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Best Local Similarity
Matches 88; Conserva
Best Local Similarity
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LENGTH: 982
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                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: EARAN, Mirko
APPLICANT: BURNS, Thomas M.
APPLICANT: DALE, James L.
APPLICANT: HARDING, Robert M.
TITLE OF INVENTION: DNA Sequences of Banana Bunchy Top Virus
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 32.4; DB 1; Length 1109; Pred. No. 0.17; 0; Mismatches 71; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 ctgcctgattatttgaaaatcagcagggacagaataaaactg 165
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APPLICATION NUMBER: US/08/202,186 FILING DATE: 24-FEB-1994
                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                              71611/102 FIKE
                                                                                                                                                      US/08/202,186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                            IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: JEFEREY, DORALD D.
REGISTRATION NUMBER: 19,980
REFERENCE/DOCKET NUMBER: 7161:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEPHONE: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3000 K Street, N.W. Washington, D.C.
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INFORMATION FOR SEQ ID NO: 13:
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Best Local Similarity 54.3%;
Matches 88; Conservative (
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                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                             FILING DATE: 24-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1109 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy of
                                                                                                                                                          APPLICATION NUMBER:
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                                                                                               OPERATING SYSTEM:
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US-08-202-186-13
                                                                              COMPUTER:
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COUNTRY:
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FEATURE:

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64 tacgaaccccttagttatcttgggttcgaccatgtgcatgtactcgtatttgccaatgtc 123
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APPLICANT: BURNS, Thomas M.
APPLICANT: DALE, James L.
APPLICANT: HARDING, Robert M.
TITLE OF INVENTION: DNA Sequences of Banana Bunchy Top Virus
NUMBER OF SEQUENCES: 60
                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.6%; Score 32.4; DB 1; Length 1111; Best Local Similarity 54.3%; Pred. No. 0.17; Matches 88; Conservative 0; Mismatches 71; Indels 3;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,186
FILING DATE: 24-FEB-1994
NAME: JEFFERY, Donald D.
REGISTRATION NUMBER: 19,980
RESPERNCE/DOCKET NUMBER: 71611/102 FIKE
TELECOMMUNICATION INFORMATION:
TELEPONE: 202 672 5399
TELEFRAX: 202 672 5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71611/102 FIKE
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Patent No. 5756708
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INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1111 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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NAME: JEFFERY, Donald D.
REGISTRATION NUMBER: 19,980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 71
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5399
                                                                                                                   TELEFAX: 202 672 5399
TELEX: 904136
INPORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1111 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
7 TOPOLOGY: circular
US-08-202-186-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W.
CITY: Washington, D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: DNA NUMBER OF SEQUENCES: 6(CORRESPONDENCE ADDRESS:
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20007-5109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, OWEN R.
APPLICANT: WHITE, OWEN R.
APPLICANT: VENTER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REPERENCE: 24366-20007.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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Best Local Similarity 57.4%; Pred. No. 22;
Matches 58; Conservative 0; Mismatches 43; Indels 0;
                                                                                                                            Length 1111;
                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                 124 ctgcctgattatttgaaaatcagcagggacagaataaaactg 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    936 CTTCCGAAGGAAGGAATCTTTCTGAAGATCGAATAAAGTTG 977
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                                                                                                                                                                         71;
                                                                                                                         Ouery Match
Best Local Similarity 54.3%; Pred. No. 0.17;
Matches 88; Conservative 0; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/103,840A CURRENT FILING DATE: 1998-06-24 NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: June 19, 2002, 16:09:16
Job time: 15014 sec
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COTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/09103840A Patent No. 6294328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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; NAME/KEY:
; LOCATION:
US-08-202-186-24
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GenCore version 4.5

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OM nucleic - nucleic search, using sw model .

Run on: June 19, 2002, 14:04:20 ; Search time 7489.97 Seconds (without alignments) 1050.568 Million cell updates/sec
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Title: US-09-462-955B-1\_COPY\_409\_991
Perfect score: 583
Sequence: 1 ttagagtatttaaattatgc......ccccaacctctgctaaccc 583

Scoring table: IDENTITY\_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : EST:\*

!: em\_estba:\*
2: em\_estbum.\*
3: em\_estin:\*
4: em\_estin:\*
5: em\_estov:\*
6: em\_estp::\*
7: em\_estp::\*
10: qb\_est2:\*
11: qb\_htc:\*
11: qb\_qss:\*
12: qb\_qss:\*
13: em\_qss\_hum:\*
14: em\_qss\_hum:\*
15: em\_qss\_hum:\*
16: em\_qss\_hum:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

AQ089903 HS\_3001\_A AL10674 Drosophil AL92816 Archidops AC746046 HS\_2277\_A BHJ75883 004\_P\_17-AL612823 T3 end of AC418525 RPCT-11-2 BB633121 BB633121 AF034173 AF034173 AQ615572 HS\_5144\_B AL098749 Drosophil AQ121628 HS\_3089\_A AZ444169 1M0239F20 BH137680 ENTPC13TR AG167308 Pan trog1 Description SUMMARIES AZ444169 BH137680 AQ089903 AQ746046 BH175883 CNS016H0 CNS0000X CNS07IRP AG167308 CNS010B7 AI942816 12 Match Length DB Query Score 36.8 36.4 36.4 36 35.6 35.6 35.4 35.2 35.2 Result . ⊗ Ö 000

AZ397924 IM0163C12 AL667528 AL667528 AZ401897 IM0168N22 AQ228962 HS_Z012_B AQ010299 HS_Z172 B	AL067144 Drosophil AQ807176 HS_3249_A AG167164 Pan trog1 AZ31069 1M0056P10 AO488982 RPCT-11-2		AQ632834 RECI-II-4 AQ728714 RE_5462_B AQ481591 RPCI-II-2 AQ077737 CIT-HSP-2 A1065300 TENU2187	AQ348508 RPCIII-11 AI226907 uj11b01.y AQ624335 HS_2103_B AQ565229 HS_5355_B AQ565203 HS_5355_B	
AZ397924 AL667528 AZ401897 AQ228962 AQ010299	CNSOODBS AQ807176 AG167164 AZ331069 AQ488982	CNS012PA BE779656 AQ008775 BG006561	AQ032834 AQ728714 AQ481591 AQ077737 AI065300	AQ348508 AI226907 AQ624335 AQ565229 AQ565203	
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## ALIGNMENTS

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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 512)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                   GSS 22-SEP-1998
              HS_3089_A1_B03_MF CIT Approved Human Gnomic Sperm Library D Homo sapiens genomic clone Plate=3089 Col=5 Row=C, DNA sequence.
AQ121628 AQ121628 GS:3498794 GSS.
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/db_xref="taxon:9606"
/db_are="plate=3089 Col=5 Row=C"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                   Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 3089 row: C column: 5
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Tripodis,N. and Ragoussis,J.
Generation of a transcription map in the region immediately centromeric to human MHC across the 6p21.2-6p21.3 chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1529 WKYRKYKKYTSTYYKSWSRWYWYTTYTWYCWCCTSMKSASCAMMRWMGYMGSRSSRSYW 1588
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599 t 149 others
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Best Local Similarity 16.7%; Pred. No. 1.1;
Matches 32; Conservative 85; Mismatches 75; Indels
                                                               DB 12; Length 512;
   2 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Tripodis, Nikos
Division of Medical and Molecular Genetics
                                                           6.9%; Score 40; DB 12
59.8%; Pred. No. 0.13;
tive 0; Mismatches
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619 c 470 q 5
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/map="6p21.3"
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High Throughput Sequencing Center
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
Library availability, please contact Pieter de Jong
(pieter@dejong.mad.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 720 row: D column: 3
Seq primer: 2866
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Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of ECORI and ECORI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at ECORI sites"

10 corpus 113 t 20 others
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACN03M07 of DrosBAC library from Drosophila melanogaster (fruit
AQ615572 15-JUN-1
HS 5144_B1_B02_SP6E RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=720 Col=3 Row=D, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Mahairas GG, Wallace JC, Hood L
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                                                                                                                                                                                                                                          Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                              Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A2444169 507 bp DNA linear GSS 04-OCT-20C IM0239F20F Mouse 10kb plasmid UUGCIM library Mus musculus genomic close UUGCIM0239F20 F, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              665 TMNNNCMNMKANTMMNMNKMMCMNNMMNNTNMKNNNNMMNNMMNNMNNNNMMNKTNKG 724
                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. I (bases 1 to 787)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Drosophila melanogaster"
/plasmid="pBelobAC11"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative 109; Mismatches 215;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.2%; Score 36.4; DB 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="DrosBAC"/clone="BACN03M07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="end : T7"
                                            Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ444169.1 GI:10592981
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Matches 10; Conservative 1
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                       ruit fly.
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonocleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xil0-Gold (Stratagene) cells and selected for ampicillin resistance."
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., Moise, wholes,R.
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                                                                                                                                                                                                                                                                                                                                              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab host="E. Coli strain XLIO-Gold, T1-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                           Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 tgtgcatgtactcgtatttgccaatgtcctgcctgattatttgaaaatcagcagggacag 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         364 TATICAIGAACTAGAAATIGGGAAAGCATITCTCTATIAATTAIGAATCAGTAGCCAIAI 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0239 row: F column: 20
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/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0239F20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 507
Location/Qualifiers
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BH137680
BH137680.1 GI:15096741
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                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 801 585 5606
                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 801 585 7177
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Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 318)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="plate=3001 Col=8 Row=O"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
                                                                                                                                                                                                    Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
                                                                                                                                                                                                                                                                                                                      High Throughput Sequencing Center University of Washington University of Washington Voll Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3818 Fax: (206) 616-3887 Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                              Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                            scanning the human genome
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Class: BAC ends
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KEYWORDS
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/db.xref="taxon:5759"
/db.xref="taxon:5759"
/clon_lib="Entamoeba histolytica Sheared DNA"
/clon_lib="Entamoeba histolytica Sheared DNA"
/note="vector: PH051: Site_1: Bst I; Constructed at The
/note="vector: PH051: Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. parasitol.
77.450.). The DNA was mechanically sheared to give a
tight size distribution (-2 kb). The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                   Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
                                                                                                        Loftus, B., Wang, Z., Van Aken, S. and Fraser, C. Determination of clone end sequences from Entamoeba histolytica HMI:IMSS sheared DNA library (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 tgaaaatcagcaggacagaataaaactgtggaatatttaaagtatgtgtcatctaaatt 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        666 ATGCCAAGATATAATAAAGTAATTATATGATAATTCAAGTACTCATTTACAACAACAAGT 607
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 36; DB 12; Length 929;
Pred. No. 3.2;
0; Mismatches 95; Indels
                                                                                                                                                                                               Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 9543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Entamoeba histolytica"
                                              Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 929)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence start: 17
High quality sequence stop: 683.
Location/Qualifiers
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Seq primer: M13-Reverse
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                          Entamoeba histolytica.
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                                                                                                                                                                                   Unpublished (2001)
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                         BACNIÉB20 of DrosBAC library from Drosophila melanogaster (fruit
                                                                                                                                               212 GITCTGGCCAGGGCAATCAGGCAGGAAGGAAATAAAGGGTAITTAAITAGGAAGAGGA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                    Gaps
                                                                       34 gttaagaacagggcattcagttcggacaaatacgaaccccttagttatcttgggttcgac 93
                                                                                                                                                                                                                                                                                                                                                                  CNS016H0 1101 bp DNA linear GSS 26-J
                                  ő
Length 318;
                                  Indels
                                  59;
DB 12;
                Pred. No. 2.6;
0; Mismatches
Score 35.6;
                                                                                                                                                                                                                                                                                                                                                                                                           fly), genomic survey sequence. AL106734
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  6.18;
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Genoscope.
                Best Local Similarity 54.6%;
                                      71; Conservative
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GSS 26-AUG-1998

318 bp DNA linear GSS 26-AUG-199 HS\_3001\_A2\_H04\_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3001 Col-8 Row=O, DNA sequence. AQ089903 GI:3458814

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- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDCP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
; Cyprinidae; Danio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          726 DGGGCGAACAGYKTADTGATATGRKAKRSGAARGGWKTGRTGTRRTATWGGDRKAGW 785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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fc67b05.xl Zebrafish WashU MPIMG EST Danio rerio cDNA clone
IMAGE:3726417 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                    342 others
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                                                                                                                                                                                                                                                        /organism="Drosophila melanogaster"
/plasmid="pbeloBAG11"
/db_xref="taxon.7227"
/clone_lib="DrosBAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.1%; Score 35.6; DB 12; 30.1%; Pred. No. 4.7;
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Unpublished (1998)
Contact: Stephen L. Johnson
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                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                 /clone="BACN16B20"
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Matches 59; Conservative
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Fax: 314 286 1810
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 488)
Salanoubat, M., Choisne, N., Artiguenave, F., Brottier, P., Wincker, P., Samson, D., Saurin, W., Weissenbach, J. and Quetier, F.
Missouri (web address: www.genomesystems.com) (email contact: Info@eqnomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequenced to assess clustering parameters or single clones
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         data were used to computationally cluster CDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were
                                                                                                                                                                                                                                                                                                                                             /tissue_type="26 somite embryos, adult livers, shield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 gaacccttagttatcttgggttcgaccatgtgcatgtactcgtatttgccaatgtcctg 126
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/lab_host="XL1-blue MRF"
                                                                                                                                                                                                                       /organism="Danio rerio"
/db_xref="taxon:7955"
                                                                                                                                               High quality sequence stop: 443 Location/Qualifiers
                                                                                                 www.rzpd.de)
Seg primer: T7 ET from Amersham
                                                                                                                                                                                                                                                                       /clone="IMAGE:3726417"
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Best Local Similarity 50.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #82277_A2_F11_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2277 Col=22 Row=K, DNA sequence.
AQ746046
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                                                                                                                    Direct Submission
Submitted (25-UUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3618 Tex: (206) 616-3618 Center Name North Center Name Natural Center Name Natural Center Natural Center Name Natural Center Natural Natural Center Natural Natural Center Natural 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 TCTTTTATCAACGACGGGTTTACCAAAGAGAGAGAGAAATACTAGATCACTTGATTTC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    207 TIGIGIGACACTCTACATGTATTGAATTGTTTCCAATTTACTTAACTTAAGAAAATGAGT 266
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Best Local Similarity 47.2%; Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                        1. .488
/organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                                                                                                           /strain="Columbia"
/db_xref="taxon:3702"
/clone_lib="IGF"
/clone="F10F11"
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88 c 87 g
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Striggidida; Schistosomatoidea; Schistosomatidae; Schistosoma.

1 (bases 1 to 524)

Le Paslier, M.-C., Pierce, R.J., Merlin, F., Hirai, H., Wu, W., Williams , D.L., Johnston, D., Loverde, P.T. and Le Paslier, D.

Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library

Genomics 65 (2), 87-94 (2000)
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Fax: (33) (0)3 20877888
Email: Raymond.Pierce@pasteur-lille.fr
CNS sequencing ID-DG0AA004CH09BP1 Bases 1-130 have 86% identity to S.mansoni EST A19749781. from base 292-163. Bases 283-408 have 84% identity to S.mansoni EST A13947831. from base 448-326.
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/note="Vector: pBeloBAC II; Site="I: Hind III; Partially
Hind III digested and size-selected S. mansoni cercarial
DNA was ligated into Hind III digested pBeloBAC 11 vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BHI75883 524 bp DNA linear GSS 29-OCT-20
004_P_17-rev SmBAC1 Schistosoma mansoni genomic clone 004P17 5',
DNA sequence.
                                                   /clone_lib="CIT Approved Human Genomic Sperm Library D" /sex="male"
                                                                                                                               /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         394 GAAGTCAAATTGTCCCTGTTTGCAGATGACTGTATATTTAGAAAACCCCATTGTC 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                       334 GITCIGGCCAGGGCAAICAGGIAGGAGAAAGAAAIAAACGGIAITCAAITAGGAAAAGAG 393
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                                                                                                                                                                                                                                                                                                                                                                                                    34 gitaagaacagggcattcagttcggacaaatacgaacccttagttatcttgggttcgac 93
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rue du Professeur A. Calmette, 59019-Lille, France
                                                                                                                                                                                        223 others
                                                                                                                                                                                                                                                                                                                                                       53;
                   /db_xref="taxon:9606"
/clone="Plate=2277 Col=22 Row=K"
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55.8%; Pred. No. 5.6;
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/organism="Homo sapiens"
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Location/Qualifiers
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/db_xref="taxon:6183"
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/sex="mixed"
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Contact: Pierce RJ
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Best Local Similarity
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and used to transform E. coli DH10B. The complete library contains 23808 clones from 4 independent sizing-ligation-transformations. Average insert size ranges from 70-127 kb and genome coverage is 7.9-fold."
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Submitted (05-0CT-2001) Genoscope - Centre National de Sequencage :
Bright 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr - Web : www.genoscope.cns.fr)
Partially Hind III disested and size-selected S. mansoni cercarial DNA was ligated into Hind III digested pBeloBAC II vector and used cloranged form E. coli DH10B. The complete library contains 23808 clones from 4 independent sizing-ligation-transformations. Average insert size ranges from 70-127 kb and genome coverage is 7.9-fold.
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T3 end of clone 004CH09 of library SMBAC1 from strain Puerto-Rican
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Le Paslier, M.C., Pierce, R.J., Merlin, F., Hirai, H., Wu, W., Williams, D.L., Johnston, D., Loverde, P.T. and Le Paslier, D. Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library
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                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                   Score 35; DB 12; Length 524;
Pred. No. 5.1;
4; Mismatches 65; Indels
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50.0%; Pred. No.
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Schistosoma mansoni
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                                                            RPCI-11-20318.TV RPCI-11 Homo sapiens genomic clone RPCI-11-20318,
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Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu,. Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genet cs (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
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Primates; Catarrhini; Hominidae; Homo.
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
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                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
Other_GSSs: RPCI-11-20318.TJ
Other_GSSs: RPCI-11-20318.TJ
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Fax: 301 838 0208
                                          linear
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/db_xref="taxon:9606"
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/sex="Male"
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Location/Qualifiers
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                 555 bp DNA linear GSS 23-MAR-1999
RPCI-11-203C8.TV RPCI-11 Homo sapiens genomic clone RPCI-11-203C8,
AQ417598
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Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
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/organism="Homo sapiens"
/db_xref="GDB:7577623"
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US-09-462-955B-1\_COPY\_611\_991 381

Title: Perfect score:

Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

Scoring table:

Searched:

- nucleic search, using sw model

OM nucleic

Run on:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

GenBmbl:\*

1: 90\_ba:\*

2: 90\_htg:\*

3: 90\_om:\*

3: 90\_om:\*

90\_om:\*

90\_ph:\*

90\_ph:\*

90\_ph:\*

em\_fun:\* em\_hum:\* em\_in:\*

gb\_sy:\* gb\_un:\* gb\_vi:\* em\_ba:\*

em\_pat:\* em\_ph:\*

em\_sts:\* em\_pl:\* em\_ro:\*

em\_vi:\* em\_un:\*

em\_om:\*

еш\_оv:\*

em\_mu:\*

length: 0 length: 2000000000

Minimum DB seq Maximum DB seq

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AR172770 Sequence
M29963 Coconut fol
AL44127 Human DNA
AC090043 Homo sapi
AL137787 Human DNA
L48038 Structure o
AC000026 Homo sapi
                                                                                         AC102175 Mus muscu
AC025672 Homo sapi
AC068523 Homo sapi
AC068734 Homo sapi
AL672059 Mus muscu
AP001312 Arabidops
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                                                                                     U86144 Influenza A
                                                                                                                                                       AC104025 Homo sapi
AL133638 Homo sapi
AL050288 Homo sapi
AX082319 Sequence
BC000719 Homo sapi
AK027763 Homo sapi
                                                  AC002059 Homo sapi
                                                                AC098157 Rattus no
                                                                      AL450164 Human DNA
AC055787 Homo sapi
                                                                                                                                   Z70206 Caenorhabdi
AL590139 Human DNA
AP002399 Homo sapi
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Rohde, W., Becker, D., Randles, J.W., Hehn, A. and Salamini, F. Use of a virus DNA as promoter
Patent: US 63345-A 116-COT-2001;
Location/Qualifiers
1. 1291
                                                                                                                                                                                                                                   AX145392
AF269816
                                                                                                                                                                                                                                                 AX145134
AB023160
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AX144954
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AC093320
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                                                                                                                                                                                                                                                                                                                                                                  Sequence 1 from patent US 6303345.
AR172770
AR172770.1 GI:17912261
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AL590139
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AC104025
HSM801507
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AX082319
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                                          June 19, 2002, 15:43:34; Search time 5904.86 Seconds (without alignments) 1350.245 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                     1 atacccgcccacgcccacgcgc......sccccaacctctgctaaccc 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                                                        3595312
  GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                       1797656 seqs, 10463268293 residues
                                                                                                                                   Total number of hits satisfying chosen parameters:
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SUMMARIES

Query Match Length DB

Score

Result NO.

em\_htg\_hum:\*
em\_htg\_inv:\*
em\_htg\_other:\* em\_htgo\_inv:\*

Homo sapi Homo sapi

Human DNA

Rhodomonas

Sequence Staphyloc Sequence Staphyloc

Staphyloc

Homo sapi

Mycobacte Mycobacte

Human DNA Oryctolag Mus muscu

Homo sapi Arabidops

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Seguence Sequence

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100.0%; Pred. No. 1.4e-75;
tive 0; Mismatches 0;
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/db_xref="GI:323312"
                                                                                                                                                  /protein_id="AAA42898.1"
                                                                                                    complement(823. .987)
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/note="ORF 4"
         /note="ORF 3"
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TGORHLOGFIHLKTGRRLOGLKTVLGNDRIHLEPTRGSDEONRDCSKRVLLEHGVP
TREVWRRENAGRFAEEPDELALEDEGGYRRCVVHGASVEWTRWAAENPFFPYHNWO
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DPKRNLILDVPRCNLEYLNYALLECVKNRRAFSSDKYEPLSYLGFDHVHVLVFANVLPD
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/translation="MEMGTDFORPILSIPPKLRVQRIFGIRLGLPGGVHQVPQQIVGP
IVAF"
                                                                                                                                                                                                                                                                                                                                                                                         circular VRL 02-AUG-1993
 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                       circular; complete genome.

Coconut foliar decay virus DNA, clones NMORG, pORG, and pORGSAU3A.

Coconut foliar decay virus

Viruses; ssDNA viruses; Nanovirus.

1 (bases 1 to 1291)

Rohde, W., Randles, J.W., Langridge, P. and Hanold, D.

Nucleotide sequence of a circular single-stranded DNA associated

With coconut foliar decay virus

Virology 176, 648-651 (1990)
                                                181 accaetttccaegtcaccaatccaggtgagtagettgetggagaagaaageegeaageet 240
                                                                                           cctgggaggtgctacccggccgaaggccgggaacaatatgaatcgagttatgggcggggc 120
   Gaps
                                1 ataccogcccgcccacgcgctatcgtttacatcttatgaatatcctgcccaggccgaagg 60
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    ö
                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Coconut foliar decay virus"
/db_xref="taxon:12474"
                                                                                                                                                                                                                                                                                                                                                                                                           Coconut foliar decay virus, complete genome.
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    0; Mismatches
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KEYWORDS
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Human DNA sequence from clone RP11-29716 on chromosome 13, complete sequence.
/protein_id="AaA42897.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1001 ATACCCGCCCACGCGCTATCGTTTACATCTTATGAATATCCTGCCCAGGCCGAAGG 1060
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corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL: Sw:, SWISSPROT: Tr:, TREMBL: WP:, WORMPEP: Information the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -INTERNAL repeat: matches 42. .880 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                        http://www.sanger.ac.uk/HGP/Chrl3
RP11-29716 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="Charlie5 repeat: matches 2373, .2585 of consensus"
                                                                                                                                                                                                                                  Emi., EMBL; SW:, SWISSPROT: Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 constructed by the Sanger Centre Chromosome 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence is the entire insert of clone RP11-29716 The true left end of clone RP11-207D10 is at 130589 in this sequence. The true right end of clone RP11-272L14 is at 88495 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="mily repeat: matches 1. .302 of consensus"
15743. .16019
/note="MLT1D repeat: matches 190. .505 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7204. 9248
/note="15 copies 3 mer gtt 75% conserved"
10198. 10397
/note="MER20 repeat: matches 7. 21% of consensus"
/note="MSTD repeat: matches 1. 394 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "note="MLTID repeat: matches 40. .482 of consensus"
9077. ,19259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            // force - Alusq repeat: matches 1. .297 of consensus" 2567. .25831
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/note="AluY repeat: matches 1. .303 of consensus"
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8333. .28578
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/note="9 copies 4 mer acac 100% conserved"
27856. .28166
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/db_xref="taxon:9606"
/chromosome="13"
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/note="70 copies 2 mer
3453, .3755
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/clone_lib="RPCI-11.2"
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/note="37 cor
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16727. .1776
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//note="12 repeat: matches 2672. .2749 of consensus" 32012. .32087
/note="11ME2 repeat: matches 6058. .6131 of consensus"
                                                                                                                                                                                                                                                                                                                                                                      Assembly confirmed by restriction digest."
                                                                                                                                                                                                                                                                                                                                                                                                                                                 //orde="MIR repeat: matches 15. .257 of consensus"
34151. .34515
//orde="LiM4 repeat: matches 4316. .4702 of consensus"
34520. .34746
//orde="MIRTA1 repeat: matches 143. .365 of consensus"
34756. .34890
//orde="MIRTA1 repeat: matches 3. .138 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34891. .35118
//note="MLTIA1 repeat: matches 162. .365 of consensus" 35316. .35546
//note="MLTIA1 repeat: matches 133. .365 of consensus"
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/note="MER02B repeat: matches 147. .626 of consensus" 39732. .40157
/note="THENC repeat: matches 1. .426 of consensus" 40158 .40295
/note="MER02B repeat: matches 1. .148 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46466. .46695
/note="MER45C repeat: matches 714. .952 of consensus"
47322. .47737
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/note="MLTH repeat: matches 448. 531 of consensus"
/note="MLTH repeat: matches 231. 269 of consensus"
/note="MLTHG repeat: matches 231. 269 of consensus"
44516. 44571
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                                                                                                      /note="L2 repeat: matches 2056. .2275 of consensus" 30667. .30744
                                                           /note="L2 repeat: matches 1508. .1650 of consensus"
30170. .30368
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/note="MLTIC repeat: matches 1. .497 of consensus"
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                      /note="MIR repeat: matches 66. .259 of consensus"
29712. .29855
                                                                                                                                                                                                                                                                                                                                                                                                          /note="MIR repeat: matches 85. .148 of consensus"
33747. .33968
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                                                                                                                                                                                                                                                                                             /note="73 copies 2 mer cc 63% conserved"
32623. 32754
/note="Sequence from overlapping clone bA272Ll4
                                                                                                                                                                                                                                                           /evidence=not_experimental 32558. .32703
                                                                                                                                                                                                               32363. 33462
/note="CpG island"
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Website:http://hgc.igtp.ac.cn
http://www.genomics.org.cn
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/clone="RP11-551L4"
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                                                                                                                                                                                                                                                                                                                                                                                 Contact: hgc@igtp.ac.cn
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Bao,J., Bao,Q., Bao,W., Bian,X., Cao,T., Chen,C., Chen,J., Ding,H.,
Dong,W., Fan,H., Peng,X., Gong,J., Guan,Q., Gu,X., Guo,D., Guo,Z.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                    48579. 49021
/note="LIMC4 repeat: matches 7494. .7944 of consensus"
49719. .50097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257 tgtttttgcgcgatcggacggctgagttgatctggcgccaaaaacctctgctaagtcccg 316
                                                                                                                                                                                                                                                                                                                   /note="LiM4 repeat: matches 5213. .5403 of consensus" 54288. .54498
/note="LiM4 repeat: matches 2146. .2357 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57716. .58679
/note="L2 repeat: matches 1725. .2750 of consensus"
59166. .59480
'note="MLT1J repeat: matches 300. .497 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                    55170. 55244
/note=""HAL1 repeat: matches 657. .731 of consensus"
                                                                                                                                                                                                                 52199. .52679 /
/note="MER31B repeat: matches 1. .477 of consensus"
53397. .53598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="TIGGER2 repeat: matches 2. .65 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACO90043 173848 bp DNA linear PRI 11-F
Homo sapiens chromosome 3 clone RP11-551L4 map 3p, complete
                                                                                                                                                                                                                                                                           /note="MER53 repeat: matches 4. .189 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Alusc repeat: matches 5. .308 of consensus" 5584. .57221
/note="L2 repeat: matches 951. .1725 of consensus"
                                                                                                                                                                       11658. .52040
note="THELC repeat: matches 1. .371 of consensus"
                                                                                  /note="THEIC repeat: matches 3. .371 of consensus"
50098. .51657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DD 161443 TGCGTAACATCTTTAACCAAGTGCCAGGCTTTCACCCTGCTGTCATCGCACC 161495
                                                                                                                            /note="THEIC-internal repeat: matches 1. .1580 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                317 tgctaagtataaatagccgcggggggctagtattacccccggggctccccaacc 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.7%; Score 37; DB 9; Length 210115; 50.9%; Pred. No. 4;
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0; Mismatches · 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="91 copies 2 mer tt 56% conserved"
5670. .55969
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Unpublished
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                                                                                                                                                         consensus"
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Matches 88; Conserv
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JOURNAL
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PRI 11-DEC-2001
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He,L., Hu,S., Huang,F., Jin,Y., Kang,N., Li,C., Li,C., Li,F.,
Li,G., Li,J., Li,L., Li,S., Li,T., Liu,X., Liu,N., Liu,B., Liu,X.,
Li,W., Li,W., Li,Y., Luo,C., Luo,J., Niu,Y., Qi,Q., Qi,X., Song,L.,
Song,S., Sun,M., Sun,W., Sun,W., Tao,R., Tao,R., Wang,H., Wang,J.,
Wang,J., Wang,J., Wang,L., Wang,L., Wang,R., Wang,X., Wang,X.,
Wu,D., Wu,D., Wu,O., Xie,F., Xuan,Z., Xue,Y., Yan,Z.,
Yu,S., Zhang,X., Zhang,G., Zhang,H., Zhang,L., Zhang,M.,
Zhang,X., Zhang,Y., Zhang,Y., Zhang,Y., Zhang,R.,
Yu,J. and Yang,H.
                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (11-PEB-2001) Human Genomic Center, Institute of
Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
100101, P.R.China
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B9446 bp

DNA

linear PRI 11-DEC-2C

Human DNA sequence from clone RP5-1070B1 on chromosome Xq22.1-23

contains the 3' end of a novel gene similar to KIAA0316 and

KIAA0967 proteins, the 5' end of the PRPS1 (phosphoribosyl

pyrophosphate synthetase 1) gene, complete sequence.

AL137787
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HTG; KIAA0316; KIAA0967; phosphoribosyl; PRPS1; pyrophosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 9; Length 173848;
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Consensus quality: 829 bases at least 030
Consensus quality: 1046 bases at least 020
Insert size: 1157; sum-of-contigs
Quality coverage: 1.35x in 020 bases;sum-of-contigs
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Chemistry: Dye-terminator: ET 55% of reads
Chemistry: Dye-terminator Big Dye: 45% of reads
Chemistry: Dye-terminator Big Dye: 45% of reads
Assembly program: Phrap; version 0.990329
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0; Mismatches
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Center project name:1% project
Center clone name: RP11-551L4
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/db_xref="taxon:9606"
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.0854. .10980
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                                                                                                                                                                                                                                                                          Submitted (10-DEC-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: hunquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Oct 20, 2000 this sequence version replaced gi:10715746.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with a note of the overlapping clone, as we submit sequences with only a small overlapping clone, as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em.; EMBL; w.; SWISSPROT; Tr., TREMBL; Wp.; WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/G_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/ChrX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >-30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RPS-1070B1 is from the library RPCI-5 constructed by the group of Pieter de Jong. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Processin_id="Cad18891.1"

/db_xref="G1:17644235"

/db_xref="G1:1764425"

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/db_xref="G1:1764425"

/db_xref="G1
                                        Eukaryota, Metazoa; Chordata, Craniata; Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(<2427. .2558,4017. .4136,9889. .10025,10359. .10485,
[2743. .12832,14519. .14698,25947. .26091,46953. .47774,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMPORTANT: This sequence is not the entire insert of clone RP5-1070B1 It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true right end of clone RP5-1070B1 is at 89446 in this sequence. The true right end of clone RP1-3D11 is at 100 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              jóin (2427. 2558,4017. 4136,9889. 10055,10359. 10485,
12743. 12822,14519. 14698,25947. 26091,46953. 47774,
49935. 53005)
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/product="dJ1070B1.1 (similar to KIAA0316 and KIAA0967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MER20 repeat: matches 1. .175 of consensus"
2066. .2119
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/codon_start=1
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http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="RP5-1070B1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="dJ1070b1.1"
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                                                                                                                                                    (bases 1 to 89446)
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                                                                                                                                                                                                                                                Direct Submission
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                                                                                                                                                                                             Bird, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat_region
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                                                                                                                                                                                                                                      TITLE
JOURNAL
                                                                                                                                          REFERENCE
                                                                                                                                                                                             AUTHORS
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EMSLRAATSSLEEDOVSELRDMLPKEVRLSPKLILDPKSSVTPALISAALQOVVHNKS
LVTAGGALGRPPSKGERRLEASMGRPEVSMASSASKNLKRKISPSAPETSMNSOHOL
GAEVSSPRAPTGSRADSLHSQOEDSLPVONPPPKSYLLTRYBESVGKQATGEVAGK
GGPVGGRPTLOKQGTISSQGEKAQLESTPKRSKLEETSLVPRATYPRALOSPSCOSRS
SEGPVGGRPTLOKQGTISSQGEKAQLESTPKRSKLEETSLVPRATYPRALOSPSCOSRS
SEGPAKPKSSRGPFRLRNLESATFPTRYKKETPETSQAASROVSTMPSRKLETTLNGAHST
GGELPGTEYLQPPAGRGSCOLRSSPVOOGFGMSREQRRSCOCKRTCRGGRPQATQTP
VPSLRGFERRRYLPSGRROPEAGFGSSPVOOGFGMSREQRRSCOCKRTCRGGRPQATQTP
                            ACLIAGYCRLLLDSRKMVFSRPASQPLPPPM1KADYMHSAHRPVTGGHLGKKESSYVG
SVGTSPRKSSRCTPPPADSELVSFCYLHMREQRKEQESRTDVNENL1FFEETRPRTKS
                                                                                            DPTSKSSGQGYEVVPDDFDAASLDHEPCASRARSYTLDNSIGAEALNFYCDSCKAKLQ
                                                                                                                           EQLGPRKGGKPGSSRDNIVDLMSLPPPGSEEEEEEEDFTTSLLPAIAAPPGFRDNSS
DEDDPRRRAVQSQEGGRHLRGLLXDEIPVTLIDSVQTRTVRDHAQELDDALVSTLQAL
                                                                                                                                                                                           EALAASEDGPHPPPPOTAGLIVLATITPESSIDSGHETNSSELTDMSEMMSAMKOHON
TTYFLAQHLNKDSLLARKDLPFRIQSCAAQAVLTAPYSLGRPDPNPSLQPIATGOSPG
PPGARRKLPQSEGGVQGERTYSLAVHPALSPQLSEQKNLSLLSPVPEDKGPGHTRAGL
ISHVIDLKTNLTTVLSEFSKISKIQLFRENQGVARVETSIMDAKPLVLLMEWPEATNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCSSSSPBASRTQEIDLRVSTFEGSLAKINALRAHAYGLPDGFLAARLDTNELLTVLR
QCVASPEARAPKPYVSQISEYKLELALKFKELRASCRRVANVDKSPTHMLAAITGSFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCASGGECLGAPNYRKLMRRYSISELDQGDRASLTSDVYPHPPLGMLPREAKEVEASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIALGPKSRSLESPTLGDPSYVQVAPETKGPRQMAVFSLPEEVYRKPAELDEDSESSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLSSLIETFVRLVFIVRSEAORQELLAKVEEVVRNYTFLLRAAEESTARNLNQQQQQ
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/note="L1ME1 repeat: matches 1754. 2088 of consensus"

6096. 7975

/note="L1ME1 repeat: matches 4322. 6163 of consensus"
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/note="LiME1 repeat: matches 4276. .4336 of consensus"
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/hote="FLAM_C repeat: matches 5. .125 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4493. .4994
/note="L2 repeat: matches 2192. .2710 of consensus"
complement(4561. .5122)
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/note="MERSA repeat: matches 18. .189 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="L2 repeat: matches 1880. .2666 of consensus" 13058. .13396 / note="MEKSB repeat: matches 1. .339 of consensus" 15045. .15353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MER5B repeat: matches 3. .172 of consensus"
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11505. .12284
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/note="Alusq repeat: matches 1. .238 of consensus" complement(8665. .8913)
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/note="MBR2 repeat: matches 1. .187 of consensus"
complement(10076. .10525)
/note="match: STS: Em:HS188B157"
10219. .10294
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'note="35 copies 2 mer aa 67% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note="38 copies 2 mer ct 64% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15356. .15389 /
/note="17 copies 2 mer aa 82% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4250. .4463
/gene="dJ1070B1.1"
/note="match: GSS: Em:AQ068401"
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/note="match: GSS: Em:AQ586861"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(3780. .4002)
/note="match: STS: Em:L24828"
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OK 73072, USA ON MAY 18, 2000 this sequence version replaced gi:3845367.

On May 18, 2000 this sequence version replaced gi:3845367.

Because these overlapping clones came from different libraries there are numerous instances of insertions, deletions, and single there are numerous instances of insertions deletions, and single acceptable polymorphisms in the overlapping regions below AC000026(58b8) 85607 12512 (0) overlaps L48038(e81f2) 1 40704 (0) AC002059(p704f1059q13) 77526 118235 (54794) overlaps L48038(e81f2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Roe, B.A. Submission Submission Submitted (01-JUN-2000) The Department of Chemistry and Chemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, The University Oval, Room 208
                                         In (bases 1 to 40709)
Peyrard,M., Pan,H.O., Kedra,D., Fransson,I., Swahn,S., Hartman,K.,
Clifton,S.W., Roc,B.A. and Dumanski,J.P.
Structure of the promoter and genomic organization of the human
beta'-adaptin gene (BAM22) from chromosome 22q12
Genomics 36 (1), 112-117 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (04-OCT-1998) The Department of Chemistry and Chemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (05-NOV-1998) The Department of Chemistry and Chemistry, the University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (01-AUG-1998) The Department of Chemistry and Chemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                              Submitted (18-FEB-1998) The Department of Chemistry and Chemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (18-MAR-1998) The Department of Chemistry and Chemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (18-JUL-1998) The Department of Chemistry and Chemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
/chromosome="22q12"
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6 (bases 1 to 40709)
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Journal 1, 20229

Journal 2, 20230

Journal 2, 20250

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18060. .18400
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/note="L2 repeat: matches 2013. .2079 of consensus"

25088. .25382

/note="Alusx repeat: matches 1. .295 of consensus"

complement(26210. .26714)

/note="match: STS: Em:HS1088P75"
                                                        /note="wirk repeat: matches 5. .172 of consensus" 16789. .16917
/note="FLAM_C repeat: matches 1. .126 of consensus" 16918. .16996
//note="wirk repeat: matches 172. .250 of consensus" 17867. .18035
                                                                                                                                                                                                                                                                                                                                             /note="1410." 18546
/note="185200 repeat: matches 2. .140 of consensus"
18553. 18584
/note="16 copies 2 mer ga 96% conserved"
18651. .18949
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20050. .20229
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Direct Submission
Submitted (01-AUG-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
           Direct Submission
Submitted (23-JUN-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (14-OCT-1998) Department Of Chemistry And Biochemistry,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (21-NOV-1998) Department Of Chemistry And Biochemistry,
The Oniversity of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
15 (bases 1 to 126312)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (13-SEP-1999) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                      Submitted (01-oCT-1998) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (05-NOV-1998) Department Of Chemistry And Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (14-SEP-1999) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
73019, USA
18 (bases 1 to 126312)
Roe,B.A.
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ON Sep 14, 1999 this sequence version replaced gi:5870977.
On Sep 14, 1999 this sequence version replaced gi:5870977.
Decause these overlapping clones came from different libraries there are numerous instances of insertions, deletions, and single nucleotide polymorphisms in the overlapping regions below.
ACO00026(58b8) 8150 126312 (0) overlaps ACO02059(p704f1059q13) 1 118230 (54799) ACO0026(58b8) 85607 126312 (0) overlaps
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (22-NOV-1998) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (15-SEP-1999) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (01-JUN-2000) Department Of Chemistry And Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                         OK 73019, USA
10 (bases 1 to 126312)
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17 (bases 1 to 126312)
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16 (bases 1 to 126312)
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Homo sapiens Chromosome 22q12 BAC Clone 58b8 In Meningioma Deletion
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Pan,H., Hartman,K., Willingham,D. and Roe,B.A.
Homo sapiens Chromosome 22q12 BAC Clone 58b8 In Meningioma Deletion
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Submitted (03-MAR-1998) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                     31651 CTTCCAGTCCCCAGCACTGTGAGAAAATAAATTCCATTGTTGAAGCCAAAAGAAAAAA 31592
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                                                0; Gaps
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On Apt 4, 1999 this sequence version replaced gi:4454595.
On Apt 4, 1999 this sequence version replaced gi:4454595.
Eccause these overlapping clones came from different libraries there are numerous instances of insertions, deletions, and single nucleotide polymorphisms in the overlapping regions below.
ACCORD (58B8) 8150 12612 (0) overlaps ACOC2059(p704f1059q13) 1 118230 (54799) ACOC2059(p704f1059q13) 77526 118235 (54794) overlaps L48038 (e8162) 1 47009 (0) ACOC2059(p704f1059q13) 136102 173029 (0) overlaps ACOC00041(p42h1) 1 36931 (8506).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (23-MAR-1999) Department Of Chemistry and Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
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                                                                                                             Submitted (17-OCT-1998) Department Of Chemistry and Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                       Submitted (30-OCT-1998) Department Of Chemistry and Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                          Submitted (22-NOV-1998) Department Of Chemistry and Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (07-JAN-1999) Department Of Chemistry and Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman
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Submitted (14-JAN-1999) Department Of Chemistry,
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Roe, B.A.
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 173029)

Pan,H., Malaj,E., Guillebault,D., Nguyen,T., Peyrard,M.,

Bumanski,J.P. and Roe,B.A.

Homo sapiens Chromosome 22q12 PAC Clone p704f1059q13 In Meningioma
Deletion Region
                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACO02059 173029 bp DNA linear PRI 01-JUN-2000
Homo sapiens Chromosome 22q12 PAC Clone p704f1059q13 In Meningioma
Deletion Region, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (14-MAY-1997) Department Of Chemistry and Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (21-MAR-1998) Department Of Chemistry and Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman, OK 73019, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (18-FEB-1998) Department Of Chemistry and Biochemistry, The University of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (17-FEB-1998) Department Of Chemistry and Biochemistry,
The University of Oklahoma, 620 Parrington Oval, Room 208, Norman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 117258 CTTCCAGTCCCCAGCACTGTGAGAAATAAATTCCATTGTTGAAGCCAAAAGAAAAAA 117199
                                                                                                                                                                                                                                                                                                                                       132 attocatttggataagaacgaatctgttactttgcttgcagtgcacgcaaccactttcca 191
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                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                  9.1%; Score 34.8; I
52.8%; Pred. No. 18;
                                                                                                                                /clone="58b8"
32141 c 32072 g 30590
                   /organism="Homo sapiens"
                                      /db_xref="taxon:9606"
/chromosome="22"
                                                                             /chromosome="22q12"
/map="22q12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 117138 CGTCGCCCAGGCTGGAGTGCAG 117117
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Best Local Similarity 52.89
Matches 75; Conservative
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TITLE
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Cavalier-Smith,". Couch, J.A., Thorsteinsen, K.E., Gilson, P.,
Deane, J., Hill,D.A. and McFadden, G.I.
Direct Submission
Direct Submission
Submitted (29-MAR-1996) T. Cavalier-Smith, Botany, University of
British Columbia, #3529-6270 University Boulevard, Vancouver, B.C.
V6T 124, Canada
                                                                                                                                                                                                                                                                         132 attccatttggataagaacgaatctgttactttgcttgcagtgcacgcaaccactttcca 191
                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Cryptophyta; Cryptomonadaceae; Rhodomonas.
1 (bases 1 to 1747)
Cavalier-Smith,T., Gouch,J.A., Thorsteinsen,K.E., Gilson,P.,
Deane,J., Hill,D.A. and McFadden,G.I.
Cryptomonad nuclear and nucleomorph 18S rRNA phylogeny
                                                                                                                                                           9.1%; Score 34.8; DB 9; Length 173029; 52.8%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                     67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RAU53128 1747 bp DNA li
Rhodomonas abbreviata nuclear 185 rRNA gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Rhodomonas abbreviata"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rhodomonas abbreviata strain=CCAP 976/10.
                                                                                                                                                                                                  0; Mismatches
                                     /chromosome="22q12"
/clone="p704f1059q13"
44777 a 42908 c 42378 g 42966
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:46948"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="CCAP 976/10"
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                                                                                                                                                                                                                                                                                                                                                                                                                        Db 109056 CGTCGCCCAGGCTGGAGTGCAG 109035
                                                                                                                                                                                                                                                                                                                                                                                             192 cgtcaccaatccaggtgagtag 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhodomonas abbreviata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U53128.1 GI:1777912
                                                                                                                                                                            Local Similarity 52.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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RAU53128/C
                                                                                                                                                                                              Matches
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                                                                                             ORIGIN
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Consensus quality: 151585 bases at least Q40
                                                                                                                                                                                                                                 Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                 Project Information
                                                                                                                                                                                                                                                                                  Center clone name: CH230-75N19
                                                                                                                                                                                                                                                                                                  ---- Summary Statistics
                                                                                                                                                                                                                                                               Center project name: GGSM
                                                                                                                                                               ---- Genome Center
                                           (bases 1 to 175293)
                                                                                                                                                                                                Center code: BCM
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                          Unpublished
                                                       Worley, K.C.
        TITLE
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                                                           AUTHORS
                                           REFERENCE
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                                                                           TITLE
                                                                                                                                             COMMENT
                                                                                                                                                           0;
                                                                                                                                                                                                                   711 TAAACGGCCTGCGTCCCACTACCCTACAGTTAAGTAGAATAGGATCCCCAGGCAGAAAGG 652
                                                                                                                                                           Gaps
                                                                                                                                                                                    2 tacccgcccacgcgctatcgtttacatcttatgaatatcctgcccaggccgaaggc 61
                                                                                                                                                         .;
0
                                                                                                                        DB 8; Length 1747;
                                                                                                                                                      37; Indels
                                  'product="18S ribosomal RNA"
                                                                                                                   8.9%; Score 33.8; D
60.2%; Pred. No. 35;
Live 0; Mismatches
                                                                                                                                                                                                                                                                      495
                                                                                                                                                                                                                                                   62 ctgggaggtgctacccggccgaaggccgggaac 94
/note="PCR-amplified"
                                                    449 g
                                                  336 c
                                                                                                                                                  56; Conservative
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Best Local Similarity

Matches

RESULT

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Query Match

BASE COUNT

ORIGIN

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RS Muzny, D. M., Adans, C., Adio-Oduola, B., Ali-osman, F. R., Allen, C., Amaratunge, H. C., Act. J. R., Barks, T., Barbaria, J., Bantooks, S. L., Amaratunge, H. C., Act. J. R., Barks, T., Barbaria, J., Bantooks, S. L., Amaratunge, H. C., Act. J. R., Barks, T., Barbaria, J., Bantooks, S. L., Amaratunge, H. C., Act. J. R., Barks, T., Barbaria, J., Bantook, S. L., Amaratunge, H. C., Act. J. R., Barks, T., Barbaria, J. Banton, T. B., Burch, P. Burch, P. Burkett, C., Barcel, R. L., Byrd, N. C., Carron, T. F., Carter, P. Burkett, C., Burcell, K. L., Byrd, N. C., Cleveland, C. D., Cox, C., Coyle, M. D., Dathorne, S. R., David, R. N., Delayer, H., Davy, Carroll, L., Dederich, D. A., Delaney, K. R., Delayed, O., Cox, C., Denn, A. L., Ding, Y. John, H. H., Douthwalter, K. J., Draper, H., Dugan-Rocha, S., Durbin, K. J., Erraquto, D. Flago, N., Ford, J., Entair, C., Escotto, M., Falls, T., Gortell, J. H., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J. H., Gorrell, J. H., Havls, K. Hant, M., Havlak, P., Hanes, A., Hamilton, K., Harris, C., Harris, K., Harris, K., Harris, K., Hann, U., King, L., Korvah, J., Jula, R., Gorrell, J., H., Gorrell, J., Huber, J., Hulk, P., Hawes, A., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulk, P., Hame, J., Jula, R., Gorrell, J., Huber, J., Hulk, P., Hame, J., Jula, R., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Louiseged, H., Lozado, R., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, R., Mapus, P., Martin, R., Maylen, R., Muyen, N., Mitchell, T., Morden, R., Maylen, R., Muyen, N., Mitchell, M., Maylen, R., Maylen, R., Maylen, R., Maylen, R., Maylen, R., Pace, A., Tamerisa, R., Pecer, L., Pecer, L., Pecer, L., Pecer, L., Pere, R., Pece, R., Pato, R., Tang, H., Pece, R., Tang, H., Pece, R., Pece, R., Pece, 
        HTG 20-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission Submission Submitted (23-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                    Rattus norvegicus clone CH230-75N19, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assembly program: Phrap; version 0.990329First call to
    linear
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 61 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Consensus quality: 159096 bases at least Q30 Consensus quality: 165302 bases at least Q20 Estimated insert size: 150759; sum-of-contigs estimation Quality coverage: Ox in Q20 bases; agarose-fp estimation Quality coverage: 2.4x in Q20 bases; sum-of-contigs estimation
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LOCUS AL450164 125051 bp DNA linear PRI 24-JAN-2001 DEFINITION Human DNA sequence from clone RPI1-550L8 on chromosome 6, complete
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Matches 65; Conservative
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Submitted (13-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
On Jan 26, 2001 this sequence version replaced gi:12044654.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone and. Note that the
corresponding to the overlapping clone, as we submit sequences with
only asmall overlap as described above.

This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
ambiguous, there is an annotation using the 'unsure feature key.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL: Sw: SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP. Information
thtp://www.sanner.ac.us/Drinter/e/C janaac/wormens.mhis sequence
the property of the contract of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMPORTANT: This sequence is not the entire insert of clone RF11-55018 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RF1-250C18 is at 124952 in this sequence. The true right end of clone XX-AC002485 is at 100 in this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC055787 189278 bp DNA linear HTG 16-JUN-2000 HOmo sapiens chromosome 6 clone RPl1-667G24 map 6, *** SEQUENCING
                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tp://www.sanger.ac.uk/HGP/Chr6
11-550LB is from the library RPCI-11.2 constructed by the group
Pieter de Jong. For further details see
tp://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 64537 TGCAGCACCTCCAGAGTCCAAATGACTGAGCAGGCCTCCCTGCCAAAGAGCAGGAATAT 64478
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Surren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Saldwin, J., Barna, N., Bastlen, V., Beda, F., Anderson, S., Baldwin, J., Barna, N., Bastlen, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campoplano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Karn, L., Kan, L., Kan, L., Kan, L., Kan, L., Kan, C., Klein, J., Lanccque, K., Johnson, R., Jones, C., Kan, L., Karatas, A., Klein, J., Lanccque, K., Lamazares, R., Landers, T., Lehoczky, J., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T. M., Oliver, J., Peterson, K., Pierre, N., Plsani, C., Pollara, V., Raymond, C., Rlaymon, C., Raymond, C., Ra
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                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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All repeats were identified using RepeatMasker:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * NOTE: This is a 'working draft' sequence. It currently consists of 54 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://ftp.genome.washington.edu/RM/RepeatMasker.html
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IN PROGRESS ***, 54 unordered pieces.
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HTG; HTGS_PHASE1.
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                                                                                                                                                                                                                                            Homo sapiens
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29310 29309; god of 120.0 bp 111 rength 29310 29309; gap of 100 bp 29310 31590; contig of 2281 bp in length 31591 31590; contig of 2281 bp in length 31591 33673; contig of 1983 bp in length 35624 33773; gap of 100 bp 35729 35728; contig of 1985 bp in length 35629 35728; contig of 2138 bp in length 35629 3578; gap of 100 bp 35729 37865; contig of 2583 bp in length 40550 40549; gap of 100 bp 40550 42575; contig of 2583 bp in length 40550 42575; contig of 2583 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42576 42675: gap of 100 bp 42676 45614: contig of 2939 bp in length 45615 4514: gap of 100 bp 45715 48125: contig of 2411 bp in length 48126 48225: gap of 100 bp 100 bp 55033: contig of 2408 bp in length 55034 53919: contig of 3186 bp in length 55034 53919: contig of 3186 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               110: gap of 100 bp 772317: contig of 3307 bp in length 117: gap of 100 bp 75535: contig of 3118 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75635: gap of 100 bp
78272: contig of 2637 bp in length
78372: gap of 100 bp
82077: contig of 3705 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82078 82177: gap of 100 bp 82178 86412: contig of 4235 bp in length 86413 86512: gap of 100 bp
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86513 91421: contig of 4909 bp in length
91422 91521: gap of 100 bp
91522 96898: contig of 5377 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96899 96998: gap of 100 bp
96999 102230: contig of 5232 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102231 102330; gap of 100 bp
102331 106721; contig of 4391 bp in length
106722 106821; gap of 100 bp
106682 111047; contig of 4226 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19: gap of 100 bp 55518: contig of 2497 bp in length 16: gap of 100 bp 59036: contig of 2420 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                           26283 27734: contig of 1452 bp in length 27735 27834: gap of 100 bp 27735 27835 29209.
11966 12065: gap of 100 bp
12066 13754: contig of 1689 bp in length
13755 13854: gap of 100 bp
13855 15223: contig of 1369 bp in length
15224 15323: gap of 100 bp
15324 16734: contig of 1411 bp in length
                                                                                                                                                                                                                  18272 18371: gap of 100 bp 18372 19546: contig of 1175 bp in length 1937 1946: gap of 100 bp 19647 20910: contig of 1264 bp in length
                                                                                                                                                                                                                                                                                                                                                                                22953 23052: gap of 100 bp 23053 24765: contig of 1131 bp in length 24765 24865: gap of 101 bp 24866 25182: contig of 1317 bp in length
                                                                                                                                                                                                                                                                                                                             10: gap of 100 bp 22952: contig of 1942 bp in length
                                                                                                                                                          34: gap of 100 bp 18271: contig of 1437 bp in length
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72317: cont
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56516: con
                                                                                                                                      15324 16734: cont
16735 16834: gap of
16835 18271: cont
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Influenza A virus (A/Swine/Quebec/192/81 (SwQc81)) neuraminidase mRNA, complete cds.
U86144.1 GI:409918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97 tatgaatcgagttatgggcgggccacaataaaagattccatttggataagaacgaatct 156
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55.0%; Pred. No. 41;
tive 0; Mismatches 54; Indels 0;
              116884 121808: contig of 4925 bp in length 116884 121808: contig of 4925 bp in length 121809 121908: gap of 100 bp 121909 127934: contig of 6026 bp in length 127935 128034: gap of 100 bp 128035 134776: contig of 6742 bp in length 13477 134876: gap of 100 bp 13477 134876: gap of 100 bp 142049 142148: gap of 100 bp 142049 142148: gap of 100 bp 148978: contig of 6730 bp in length 148979 148978: contig of 6730 bp in length 148979 148978: contig of 6739 bp in length 157075 157174: gap of 100 bp 157075 157174: gap of 100 bp 165014 166013: gap of 100 bp 166014 177085: contig of 100 bp 166014 177085: contig of 100 bp 177086 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 177085 1
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Location/Qualifiers
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/clone_lib="RPCI-11 Human Male BAC"
1. .1071
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/note="assembly_fragment"
4211. 5676
/note="assembly_fragment"
5777. 6954
/note="assembly_fragment"
7055. 8467
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12066. 13754
/note="assembly_fragment"
13855. 15223
/note="assembly_fragment"
15324. 16734
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/note="assembly_fragment"
8568. .10046
/note="assembly_fragment"
10147. .11965
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1172. .2443
/note="assembly_fragment"
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/db_xref="taxon:9606"
/chromosome="6"
116783: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177086 177185: gap of
177186 189278: conti
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Best Local Similarity 55.09
Matches 66; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
JOURNAL
                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
          influenza A virus (A/Swine/Quebec/192/81 (SwQc81)).
influenza A virus (A/Swine/Quebec/192/81 (SwQc81)).
Viruses; SSRAM negative-strand viruses; Orthomyxoviridae; Influenza virus A and B group; Influenza A viruses; Influenza A virus; unidentified subtype.
1 (bases 1 to 1438)
Arora, D.J.S., Tijssen, P., Dea, S. and Henrichon, M.
Complete sequences of the neuraminidase genes of swine influenza viruse (HINI) associated with the respiratory disease in pigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MYTNORITHIGFICLIVGIVSLLLQIGNIVSLWISHSIOFGEKS
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DNSIRIGSKGDIFVMREPFISCSHFECRTFFLTQGALLNDRHSNGTVKDRSPYRTLMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WRNKILRTØESECVCINGSCFTIMTDGPSNGQASYKIFKMEKGKITKSTELDAPNYHY
EECSCYPDTGKVVCVCRDNWHASNRPWVSFDQNLDYQIGYICSGVFGDNPRSNDGKGN
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IIALTDWSGYSGSFVQHPELFGMNCIRPCFWVELIRGQPKESTIWTSGSSISFCGVNS
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 74854)
                                                                                                                                                                                                                                                                       Submitted (21-JAN-1997) CRV, Institut Armand-Frappier, 531 Boul. des Prairies, Laval, QC H7N4Z3, Canada Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC102175 74854 bp DNA linear HTG 23
Mus musculus clone RP23-477G17, LOW-PASS SEQUENCE SAMPLING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.7%; Score 33; DB 14; Length 1438; 60.7%; Pred. No. 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35; Indels
                                                                                                                                                                                                             2 (bases 1 to 1438)
Dea,S., Arora,D.J.S., Tijssen,P. and Henrichon,M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                               /strain="A/Sw/Quebec/192/81 (SwQc81)"
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Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:57280"
/note="tissue culture-adapted virus"
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0; Mismatches
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/protein_id="AAD00583.1"
/db_xref="G1:4099319"
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Adderson, S., Barna, N., Bastlen, V., Boguslavkky, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Calangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArtellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Farcier, P., DeArtellano, K., Dewar, K., Diaz, J.S., Gardyna, S., Gord, S., Goyette, M., Graham, L., Grand-Pherre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., MacCan, C., MacCan, P., McRennan, K., Merbeeters, R., Meldrim, J., Moneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Noyuen, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phukkang, P., Pierce, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Santos, R., Schuer, S., Schupback, R., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Tavars, N., Travers, M., Travers, M., Travers, M., Travers, M., Travers, N., Tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This record contains 90 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L18168
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100 bp
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100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center code: WIBR
Web site: http://www-seq.wi.mit.edu
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f 750 bp i
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8199: com
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6539: c
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18082: con.,
18082: con.,
182 gap of
18909: contig of 727 bp in ..
19009: gap of
100 bp
19719: contig of 710 bp in length
7717 pp in length
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ap of 100 bp
i. contig of 730 bp in length
gap of 100 bp
ii. of 717 bp in length
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4p of 100 c, contig of 733 bp in ...
100 bp in length
                                                                                                                                                                                                                                                              100 bp
1744 bp in length
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contig of 747 bp in length
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                                                                                                                                                                                                                                                                                 12283 12382; gap of 100 bp
12383 13126: contig of 744 bp in length
13127 13226; gap of 100 bp
13227 13922: contig of 696 bp in length
13923 14022; gap of 100 bp
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11532 3252; contig of 721 bp in length
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34882 35598: contig of 717 bp in length
10603: contig of 651 bp in length
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AC025672 167178 bp DNA linear HTG 20-SEP-2000 Homo sapiens chromosome 18 clone RP11-715F3 map 18, WORKING DRAFT SEQUENCE, 20 unordered pieces.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 167178)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57085 AAATACTATTTTTCTCCAGATAGCCAAAGCCTGTGAAGGCCCACGAGTTCCCAGAGA 57026
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Pred. No. 61;
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Best Local Similarity 49.7%;
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S Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastlen, V., Beda, F., Baldwin, J., Barna, N., Bastlen, V., Beda, F., Campoplano, A., Castle, A., Choppel, Y., Colangelo, M., Collins, S., Campoplano, A., Castle, A., Choppel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Domino, M., Doyle, M., Grereira, P., Fitzhugh, W., Gage, D., Grand-Flerre, N., Grand, S., Goyette, M., Graham, L., Gandyna, S., Ginde, S., Goyette, M., Graham, L., Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Larkoque, K., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, M., McRernan, R., Menga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Ollvar, T.M., Oliver, J., Peterson, K., Pierre, N., Flands, J., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talanas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Direct, Shhinission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 155253 bases at least Q40
Consensus quality: 165250 bases at least Q30
Consensus quality: 166256 bases at least Q20
Insert size: 176000; agarose-fp
Insert size: 155278; aum-of-contigs
Quality coverage: 4.4 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27917: contig of 27917 bp in length
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28018 29021: contig of 1004 bp in length
29022 29121: gap of 100 bp
29122 30937: contig of 1816 bp in length
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33055 33154: gap of 100 bp
33155 33154: gap of 100 bp
34155 34403: contig of 1249 bp in length
34504 35513 gap of 100 hn
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  Homo sapiens chromosome 18, clone RP11-715F3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: L8225
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COMMENT

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103580 103679: gap of 100 bp 103680 117213: contig of 13534 bp in length 117214 117313: gap of 100 bp 100 bp 117314 133144: contig of 15831 bp in length
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133245 160275: contig of 27031 bp in length
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160376 167178: contig of 6803 bp in length.
44557: contig of 4874 bp in length
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48993: contig of 4336 bp in length
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contig of 4698 bp in length
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Search completed: June 19, 2002, 15:48:13 Job time: 13751 sec

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                                                                                                                              June 19, 2002, 16:51:12; Search time 3798.65 Seconds (without alignments) 172.204 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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## ALIGNMENTS

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Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                     Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
                                                      Human cDNA sequence SEQ ID NO:15487
AAH16471 standard; cDNA; 2827 BP.
                                                                                                                                                                 28-JUL-2000; 2000EP-0116126.
                                                                                                                                                               99JP-0248036.
                                                                                                                                                                                                  2000JP-0241899
                                   26-JUN-2001 (first entry)
                                                                                                                                                                                                                     (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                 WPI; 2001-318749/34.
                                                                                                          EP1074617-A2
                                                                                                                                                              29-JUL-1999;
                                                                                                                                                                                                  09-JUN-2000;
                                                                                                                           07-FEB-2001.
                 AAH16471;
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AAH54604 standard; DNA; 3002 BP.
                                                                                                                                                                                                                                                  09-NOV-2000; 2000WO-US30782
                                                                                                                                                                                                  03-SEP-2001 (first entry)
                                                                                                                                                                                                                            Staphylococcus epidermidis
                                                                                                          of the present invention.
                                                                                                                                                                                                                                                                 (GLAX ) GLAXO GROUP LTD.
              full-length cDNAs
                                                                                                                                                                                                                                    WO200134809-A2
                                                                                                                                                                                                                                                          09-NOV-1999;
                                                                                                                                                                                                                                           17-MAY-2001.
                                                                                                                                                                                           AAH54604;
                                                                                                                                                                                 AAH54604
                                                                                                                                                                             RESULT
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Kimmerly WJ;

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AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG81120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors ontaining them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) fand/or nucleic acids) may then be containing them which are used to produce hosts cells which express the polypeptides may also be used to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the activity and therefore identify compounds that may be used for the AAH55090 represent specifically claimed S. epidermidis genomic DNA AH55091 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention. AAH55091 to sequence listing of the present specification, however the sequence listing of the SEQ ID NO:4454 so even the sequences are given in the disclosure for SEQ ID NO:4455 to 4472, on sequences are present for SEQ ID NO:4455 to 4472,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 tittgcgcgatcggacggctgagttgatctggcgccaaaaacctctgctaagtcccgtgc 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          627 atttaagtgattatettagtatagaaaatgeetgagaeaatgattgteeeaggeatttta 686
                                                                             Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S. epidermidis genomic polynucleotide sequence {\tt SEQ} ID NO:3676.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus epidermidis SRI strain; infection; diagnosis; vaccination; endocarditis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3002 BP; 899 A; 595 C; 418 G; 1090 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 32.4; DB 22;
pred. No. 0.84;
0; Mismatches 61;
                                                                                                                                                                                      Claim 8; Page 1634-1635; 2188pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.5%;
53.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GLAX ) GLAXO GROUP LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        747 tcattaccaa 756
                            WPI; 2001-316495/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
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                                                                                                                                                                                                                                                     The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide comprises one of the 5602 nucleotide sequences defined in the specification, where the coligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 1 least 15 nucleotides; or (b) a combination of sequence and an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 1'-end sequence complementary to a coligonucleotide which comprises a 1'-end sequence of oligonucleotide which represent 1'-end sequence/3'-end sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the proteins encoded by the full-length cDNAs. The primers also when the proteins encoded by the full-length cDNAs. The primers also well shall shall seasily without any specialised methods. AAH03166 to AAH13628 and AAB056803 rowresont human cDNA sequences; and anilatest and anilatest and anilatest anilat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                            Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2134 gttaggtggtttagggccaaaaggggaaaaccacttgagtcttgtggtgtgtgg 2187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64 gggaggtgctacccggccgaaggccgggaacaatatgaatcgagttatggggcgg 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S. epidermidis genomic polynucleotide sequence SEQ ID NO:3968.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2827 BP; 560 A; 791 C; 859 G; 617 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 8.5%; Score 32.4; DB 22; Best Local Similarity 55.3%; Pred. No. 0.82; Matches 63; Conservative 0; Mismatches 51;
                                                                                                                                                                                                    Claim 8; SEQ ID 15487; 2537pp + CD ROM; English.
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AAH52304 to AAH53970 represent nucleic acids (1) encoding polypeptides (11), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (1) and (11) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (1) may be used to produce the soldermidis polypeptides (11) via the production of vectors ontaining them white aced to produce hosts cells which express the polypeptides (11) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55091 represent specifically claimed S. epidermidis genomic DNA polyuncleotide sequences from the present invention. AAH55091 to AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ttttgcgcgatcggacggctgagttgatctggcgccaaaaacctctgctaagtcccgtgc 319
                                                                                       Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
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0
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    S. epidermidis genomic polynucleotide sequence SEQ ID NO:4114.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3295 BP; 971 A; 667 C; 456 G; 1201 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    no sequences are present for SEQ ID NO:4455 to 4464.
                                                                                                                                               Claim 8; Page 1285-1287; 2188pp; English.
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Matches 69; Conservative
                                                     WPI; 2001-316495/33.
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                 Kimmerly WJ;
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AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.

(II) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the used in vaccination. The nucleic acids (I) may be used to produce to vaccinate which are used to produce hosts cells which express the polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55091 to AAH55099 represent oligonucleotide sequences and primers which are used the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in the exemplification of the present invention.

N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2650 tttattggcaattgacaaccgagttgaacttgggctaatctcaatttcaactctagtcc 2709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260 ttttgcgcgatcggacggctgagttgatctggcgccaaaaacctctgctaagtcccgtgc 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                    Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3518 BP; 1091 A; 677 C; 495 G; 1255 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            no sequences are present for SEQ ID NO:4455 to 4464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.5%; Score 32.4; DB 22; 53.1%; Pred. No. 0.91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                 Claim 8; Page 1808-1809; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAH54492 standard; DNA; 3985 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vaccination; endocarditis;
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nes 69; Conservative
                GLAX ) GLAXO GROUP LTD.
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                                                                                                WPI; 2001-316495/33
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                                                           Kimmerly WJ;
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AAH52304 to AAH53970 represent nucleic acids (1) encoding polypeptides (11), given in AAG81454 to AAG8120, from Staphylococcus epidermidis. (1) and (11) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (1) may be used to produce the S. epidermidis polypeptides (11) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (11) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent oliquidis infections, e.g. endocarditis. AAH53971 to polynucleotide sequences from the present invention. AAH55091 to AAH55091 represent oliquide sequences and primers which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4455 to 4464.
                                                                                                                                                                                                           Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
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                                                                                                                                                                                                                                                                                            Claim 8; Page 1500-1502; 2188pp; English.
99US-0164258.
                                                    (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                      WPI; 2001-316495/33.
09-NOV-1999;
                                                                                                         Kimmerly WJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cytokine; cell proliferation; cell differentiation; growth factor;
                                                                                                                                                                            260 ttttgcgcgatcggacggctgagttgatctggcgccaaaaacctctgctaagtcccgtgc 319
                                                                                                                  381 atttaagtgattatcttagtatagaaatgcctgagacaatgattgtcccaggcatttta 440
                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                haematopoiesis regulation, tissue growth, immunomodulator; activin, inhibin, chemotaxis, chemokinesis, thrombolyysis, oncogenesis; proliferation, metastasis, cancer; tumour; haematopoietic disorder; myeloid cell disorder, lymphoid cell disorder; arthritis; chronic inflammatory condition, proliferative retinopathy; atherosclerosis; coronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder;
Query Match 8.5%; Score 32.4; DB 22; Length 3985;
Best Local Similarity 53.1%; Pred. No. 0.97;
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human dJ889M15.3 homologue-encoding cDNA, SEQ ID NO:567.
                                      61;
                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            ABA08791 standard; cDNA; 5651 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JAN-2002 (first entry)
                                        69; Conservative
                                                                                                                                                                                                                                     320 taagtataaa 329
                                                                                                                                                                                                                                                                            501 tcattaccaa 510
                                                                                                                                                                                                                                                                                                                                                                                                                   ABA08791;
                                        Matches
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Sequences ABB10381-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides of nucleotides of the invention. Although novel, many of the bind to polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence co potential therapeutic applications. The polypeptides of the invention have biological activities, and hence to premit a transpeutic applications. The polypeptides of the invention may have various activities; including cytokine, cell proliferation or cell differentiation activities; stem cell growth factor activity; chromodulatory activity; activin- or inhibin-related activities; chemotactic or chemokinetic activities; haemostatic, thrombotic or thrombolytic activities; reaceptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis.

Compositions, e.g., by protein or gene therapy. Such conditions and uncleotides of the invention are useful for preventing, treating or ameliorating medical disorders, haematopoletic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions, e.g., asthma or arthritis), conditions, e.g., by protein or gene therapy. Such conditions and unclearing activities arterial ischaemla, bone disorders (e.g., osteoporosis), and abnormal varelial ischaemla, bone disorders (e.g., osteoporosis), and abnormal varelial or general or metastasis.

Crepair or nucleic acids encoding them) may be used to promote wound replaing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities and beativity may be used to promote variativities and beating to multiper activities and beativity may be used to promote or polyventides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bacterial and fungal infections in addition to immune disorders.

Polypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells
tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antiinflammatory; antiathmatic; antiathritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 582-584; 1963pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                 03-FEB-2000; 2000US-0496914.
                                                                                                                                                                                                                                                                                                                                                                                                       27-APR-2000; 2000US-0560875.
                                                                                                                                                                                                                                                                                                                                05-FEB-2001; 2001WO-US03800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e.g. arthritis and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-457740/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; ABB11547
                                                                                                                                                                                                                          WO200157188-A2.
                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                              09-AUG-2001.
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Sequence 5651 BP; 1077 A; 1633 C; 1680 G; 1261 T; 0 other;

Score 32.4; DB 22; Length 5651; Pred. No. 1.1; 8.5%; Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                    antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system; virucide; antiagcegral; endocrine; cardiant; central nervous system; virucide; antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; eczema; dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic; neuroprotective; antidepressant; nootropic; antiparknosnian; infection; immunostimulant; gene therapy; antisense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cardiac dysfunction, neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; hematopoietic disorder; platelet disorder; asthma; thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                Gaps
                                          4 cccgcccacgcccacgcgctatcgtttacatcttatgaatatcctgcccaggccgaaggcct 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection -
                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cancer; ulcer; HIV infection; human immunodeficiency virus;
                                                                                                                                             64 gggaggtgctacccggccgaaggccgggaacaatatgaatcgagttatgggcgg 117
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0
      51; Indels
                                                                                                                                                                                                                                                                                                                                                                                          Human protein encoding cDNA sequence SEQ ID NO:615.
  0; Mismatches
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                                                                                                                                                                                                                                                                      BP
                                                                                                                                                                                                                                                                 AAH99780 standard; cDNA; 5653
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0471275.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-APR-2000; 2000US-0552317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurological disorder; ss
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001-457603/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAM25839
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63;
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Matches
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of disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, asteoporosis, severe combined immunodeficiancy, eczema, allergic rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression, Alzheimer's disease, Parkinson's disease, neurodegenerative and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-brager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wang D;
                                                                                                                                                                                                                                                                                                           770 CCCAGGAGCCTTCCCCATGTCCTTGCTGAGAATTGCCCTCCCATGCCGCTGAGGT 711
                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                              4 cccgcccgcccacgcgctatcgtttacatcttatgaatatcctgcccaggccgaaggcct 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acids and polypeptides, useful for treating disorders
                                                                                                                                                                                                                                                                                                                                          64 gggaggtgctacccggccgaaggccgggaacaatatgaatcgagttatgggcgg 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhang J;
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                                                                                                                                                                                                                                                                                                                                                                          710 GITAGGIGGITTAGGGCCCAAAAGGGGAAAACCACTIGAGTCTIGTGGTGTGTGG 657
                                                                                                                                                                                                              Length 5653;
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                                                                                                                                                               Sequence 5653 BP; 1262 A; 1680 C; 1632 G; 1079 T; 0 other;
                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yang Y,
                                                                                                                                                                                                                                              51;
                                                                                                                                                                                                                8.5%; Score 32.4; DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu C, Asundi V, Chen R, Ma Y,
Wang Z, Wehrman T, Xu C, Xue AJ,
Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                 Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              such as central nervous system injuries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human polynucleotide SEQ ID NO 4843.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAI60854 standard; cDNA; 5653 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0488725.
2000US-055317.
2000US-0598042.
2000US-0620312.
2000US-0653450.
                                                                                                                                                                                                                             55.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-DEC-2000; 2000WO-US34263
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2000US-0693036.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                              Conservative
                                                                                                                                 neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-442253/47.
P-PSDB; AAM41698.
                                                                                                                                                                                                                             Best Local Similarity
Matches 63; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     leukaemia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-OCT-2001
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09-JUL-2000;
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                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAI60854/c
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Claim 1; SEQ ID NO 4843; 10078pp; English.

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              The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                       system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, parkinson's disease, Huntington's disease, auch as alteral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, activity, chemoteatic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antinflammatory; antirheumatic; antiarthritic; immunosuppessive; antibacterial; endocrine; cardiant; central nervous system; virucide; antibacterial; endocrine; cardiant; central nervous system; virucide; antiangement; hacmostatic; vulnerary; antiulcer; osteopathic; cezema; dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic; neuroprotective; antideperssant; nootropic; antiparkinsonian; infection; immunostimulant; gene therapy; anticense therapy; vaccine; inflammation; antianaphylactic; rheumatoid arthritis; septic shock; pancreatitis;
                                                                                                                                                                                                                                                                                                                                          The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity; genetic disease; haematopoietic disorder; platelet disorder; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thrombocytopaenia; osteoporosis; severe combined immunodeficiency; allergic rhinitis; diabetes; multiple sclerosis; depression; Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 eccgecegeceaegegetategtttaeatettatgaatateetgeeeaggeegaaggeet 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  770 cccassascerrececarsrecerrecerrecasaarrscerecarsesser 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64 gggaggtgctacccggccgaaggccgggaacaatatgaatcgagttatgggcgg 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             710 GITAGGIGGITTAGGGCCAAAAGGGGAAAACCACTIGAGICTIGIGGIGIGIGG 657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.5%; Score 32.4; DB 22; Length 5653; 55.3%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5653 BP; 1262 A; 1680 C; 1632 G; 1079 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human protein encoding cDNA sequence SEQ ID NO:331.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH99496 standard; cDNA; 5654 BP.
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21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neurological disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                       C.N.S disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200153455-A2.
                                                                                                                                                                                                                                                                                                                                                              specification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH99496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                             Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
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AAH99166 to AAH99904 encode the human proteins given in AAM25225 to
AAW25963. The proteins can have activities based on the tissues and
cells they are expressed in, such as: antinifammatory; antinheumatic;
central nervous system; virucide; antibacterial; endocrine; cardiant;
cardiovascular; antianaemic; antiagegrapht; hemostatic; vulnerary;
antiulcer; osteopathic; dermatological; antiallergic; antiasthmatic;
antidabetic; cytostatic; neuroprotective; antidepressant; noctropic;
antidaphetic; cytostatic; neuroprotective; antidepressant; noctropic;
antidaphetic; cytostatic; neuroprotective; antidepressant; noctropic;
conduction, The proteins and polynucleotides are useful for screening for agonits or antagonists of a protein and for the treatment and diagnosis;
cf disorders associated with the activity of a protein e.g. inflammation, rheumatoid arthritis, septic shock, pancreatitis, cardiac daysfunction, infections, autoimmunity, genetic diseases, haematopoletic disorders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, cancer, multiple sclenosis, depression, alloring and platelet, mannade in munodeficiency, eczema, allergic
chinitis, asthma, diabetes, cancer, multiple sclenosis, depression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cytokine; cell proliferation; cell differentiation; growth factor; haematopoiesis regulation; tissue growth; immunomodulator; activin; inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis; proliferation; metastasis; cancer; tumour; haematopoietic disorder; myeloid cell disorder; lymphoid cell disorder; asthma; arthritis; chronic inflammatory condition; proliferative retinopathy; attenosclerosis; oronary heart disease; arterial ischaemia; bone disorder; osteoporosis; vascular growth disorder; tissue regeneration; wound healing; infection; immune disorder; cell culture; drug screening; gene therapy; antihifammatory; antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic; cytostatic; osteopathic; vascuropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4887 cccaggagcettececatgteettgeettgetgagaattgeeeteceatgeegetgaggt 4946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 eccgecegeceaegegetategtttaeatettatgaatateetgeeeaggeegaaggeet 63
                                                                                                                                                  Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4947 gttaggtggtttagggccaaaaggggaaaaccacttgagtcttgtgggtgtggg 5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 gggaggtgctacccggccgaaggccgggaacaatatgaatcgagttatgggcgg 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 8.5%; Score 32.4; DB 22; Length 5654; Best Local Similarity 55.3%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5654 BP; 1078 A; 1631 C; 1682 G; 1263 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human dJ889M15.3 homologue-encoding cDNA, SEQ ID NO:572.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                Claim 1; Page 444-446; 1217pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABA08796 standard; cDNA; 5665 BP
                      Tang YT, Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neurological disorders.
                                                                        WPI; 2001-457603/49.
                                                                                                   P-PSDB; AAM25555
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Homo sapiens.
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WO200157188-A2

09-AUG-2001

05-FEB-2001; 2001WO-US03800

03-FEB-2000; 2000US-0496914

27-APR-2000; 2000US-0560875

(HYSE-) HYSEQ INC.

Tang YT, Liu C, Drmanac RT;

WPI; 2001-457740/49. P-PSDB; ABB11552 Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -

Claim 1; Page 586-587; 1963pp; English.

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA08225-ABA09574 represent nucleic acids encoding them. The sequences ABA08255-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the nucleotides.

CC antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may differentiation activities; including cytokine, cell proliferation or cell differentiation activities; including cytokine, cell proliferation or cell immunomodulatory activity; activit, tissue growth activities, chemotactic or chemokinetic activities; haemostatic, thrombotic or chemotactic or chemokinetic activities; haemostatic, thrombotic or chemotactic activities; nacer cell proliferation or metastasis.

CC chemotactic or themokinetic activities; haemostatic, thrombotic or thrombotic activities; receptor or ligand activities; or may be involved in oncogenesis, cancer cell proliferation or metastasis.

CC involved in oncogenesis, cancer cell proliferation or metastasis.

CC conditions, e.g., by protein or gene therapy. Such conditions (e.g., asthma or arthritis), dispendences, haematopoietic disorders (e.g., mayeloid or lymphoid cell disorders, conditions, cell proliferation and conditions, cell or or proliferative retinopathy, atheroscilerosis, coronary heart disease, conditions, cell prowth, atheroscilerosis, coronary heart disease, cepair (or nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcrs), while those with leading (e.g., of burns, incisions and ulcrs), while those with langulates stem cells growth. Polypeptides may be used to augment autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a cDNA encoding a novel human polypeptide of the invention.

Sequence 5665 BP; 1077 A; 1634 C; 1687 G; 1267 T; 0 other;

Gaps .; 0 Query Match

8.5%; Score 32.4; DB 22; Length 5665;
Best Local Similarity 55.3%; Pred. No. 1.1;
Matches 63; Conservative 0; Mismatches 51; Indels 0;

4895 cccaggagcettccccatgtccttgccttgctgagaattgccctcccatgccgctgaggt 4954 4 occyccogcocacycyctatcgtttacatcttatgaatatcctycccaygccyaaygcot 63 ó

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Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC 1551 and H37Rv differ
                                                                                                                                                                  Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome; variation; epidemiology; patient treatment; epidemic monitoring; ds.
                     4955 gttaggtggtttagggccaaaaggggaaaaccacttgagtcttgtggtgtgtgg
64 gggaggtgctacccggccgaaggccgggaacaatatgaatcgagttatgggcgg 117
                                                                                                                                              Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 1.
                                                                                                                                                                                                                                                                                                                                          Fraser CM, Venter JC;
                                                                           AAI99682 standard; DNA; 4411529 BP.
                                                                                                                                                                                                                                                                       98US-0103840.
                                                                                                                                                                                                                                                                                             98US-0103840.
                                                                                                                                                                                                    Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                          Fleischmann RD, White OR,
                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                    (GENO-) INST GENOMIC RES
                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-647261/74.
                                                                                                                                                                                                                          US6294328-B1.
                                                                                                                                                                                                                                                                       24-JUN-1998;
                                                                                                                       15-JAN-2002
                                                                                                                                                                                                                                                25-SEP-2001
                                                                                                  AA199682;
                                                                 AA199682/c
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The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, Mycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and H37Rv (AAI99682). The method is useful for evaluating strain variation of M. tuberculosis and has valuable application in the fields of Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html?DocID=6294328Bl.

Claim 3; SEQ ID NO 1; 3pp + Sequence Listing; English.

Sequence 4411529 BP; 758565 A; 1449983 C; 1444602 G; 758379 T; 0 other;

0; Gaps 8.5%; Score 32.2; DB 22; Length 4411529; 57.4%; Pred. No. 34; 43; Indels Pred. No. 34; 0; Mismatches Conservative Best Local Similarity Matches 58; Conserv Query Match

Db 3577728 GAGCGCACGCAACAAACACCCCCGAGCTGCCGTCTGCCGTCGCGTCGCGTTGCAC 3577669 δλ

268 gatcggacggctgagttgatctggcgccaaaaacctctgct 308 δλ

0;

Db 3577668 GCACTGTTTGCCGAGCCGGCCAGGAGCGAATCCCAACTGCT 3577628

RESULT 12 AAI86825/c

AAI86825 standard; cDNA; 460 BP

197 TGCCC 193

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The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hammatopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                           cytokine; cell proliferation; cell differentiation; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     317 CTCCCATCATGCTGGGATTACAGGTGCACTCAGCCTATAAGGGGGTTTTGCCTTCCAGTTC 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          185 ctttccacgtcaccaatccaggtgagtagcttgctggagaagaaagccgcaagcctctat 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          377 CTTGATACATTGCCAAGCCTGGTCTCAAGCTTTGGCATCAAGCAATCCTCGCCCCTCAGC 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 ctaccgiccaitigitititgcgcgaicggacggctgagitgaictggcgccaaaaaccic 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tgctaagtcccgtgctaagtataaatagccgcggggggctagtattacccccgcgggctccc 364
                                                                                                                                                          vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      diagnosing and treating e.g. leukaemia, inflammation and immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acids and polypeptides, useful for preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 6885; 1399pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 460 BP; 114 A; 115 C; 141 G; 88 T; 2 other;
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Pred. No. 0.77;
0; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                      Human polynucleotide SEQ ID NO 6885.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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ilarity 48.1%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu C, Drmanac RT;
                                                                                                                                                                                                                                                                                                                                            26-FEB-2001; 2001WO-US04927.
                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2000; 2000US-0515126
                                                                                                                                                                                                                                                                                                                                                                                              18-MAY-2000; 2000US-0577409
                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                     WO200164835-A2.
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                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89;
                                                                     06-NOV-2001
                                                                                                                                                                                                                                                                                                        07-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rang YT,
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                                   AAI86825;
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of oligonucleotide comprises at least 15 nucleotides and the combination of
                                                                                                                                                Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                              Yamamoto J;
                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashi K, Saito K, Ya
A, Nagai K, Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8; SEQ ID 14725; 2537pp + CD ROM; English.
                                                                                                                      Human cDNA sequence SEQ ID NO:14725.
                                                                                                                                                                                                                                                                                                                                                                                                                              sogai T, Nishikawa T,
Sugiyama T, Wakamatsu
                            BP.
                            AAH16050 standard; cDNA; 2497
                                                                                                                                                                                                                                                                                                                       99JP-0300253.
2000JP-0118776.
2000JP-0183767.
                                                                                                                                                                                                                                                                            28-JUL-2000; 2000EP-6116126.
                                                                                                                                                                                                                                                                                                         99JP-0248036
                                                                                                                                                                                                                                                                                                                                                                    09-JUN-2000; 2000JP-0241899
                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                Isogai T,
                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                  EP1074617-A2.
                                                                                                                                                                                                                                                                                                                         27-AUG-1999;
11-JAN-2000;
                                                                                                                                                                                                                                                                                                           29-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                        02-MAY-2000;
                                                                                           26-JUN-2001
                                                                                                                                                                                                                                                 07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                Ishii S,
                                                           AAH16050;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Ota T,
13
                AAH16050/c
 RESULT
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Gaps

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Length 2497; Indels

Score 31.2; DB 22; Pred. No. 2.1; 0; Mismatches 78;

8.2%;

Query Match
Best Local Similarity 50.0
Matches 78; Conservative

the specification. The primer sets can be used in antisense therapy and the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNas. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNas. The primers allow obtaining of the full-length cDNas easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH13612 represent human cDNa sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH3612

; 0

represent oligonucleotides, all of which are used in the exemplification

Sequence 2497 BP; 732 A; 522 C; 617 G; 626 T; 0 other;

of the present invention.

Gemini virus DNA fragment stem loop.

(first entry)

10-MAY-1999

AAX02688;

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0
                                            2229 AGGCATGAGCTGCCGCACCCGGCCAAATTCTTTTAATTCTTTAGACACACGTTAGAGGGG 2170
aggoottgggaggtgotacccgggccgaaggccgggaacaatatgaatcgagttatgggcgg 117
                                   A DNA fragment from the CFDV genome can be used as a phloem-specific promoter in the construction of transgenic plants. The promoter is strong; it has 30-50% of the activity of the CaMV 35S promoter in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                           Coconut Foliar Decay Virus, CFDV; strong promoter; tissue-specific; phloem-specific; stem-loop structure; transgenic plant; ds.
                                                                                                                                                                                                                                                                                             /note= "loop has homology to geminivirus sequence"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of coconut foliar decay virus DNA as promoter - 1
tissue-specific gene expression in transgenic plants
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100.0%; Pred. No. 0.28;
tive 0; Mismatches 0
                                                                                2109 ACAGAGTCTTGCTTGTTGCCCAGGCTGGAGTGCAG 2074
                                                                                                                                                                                          Coconut Foliar Decay Virus promoter stem-loop.
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                                                                      gcaaccactttccacgtcaccaatccaggtgagtag 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   331 agccgcgggggctagtattacccccgcggct 361
                                                                                                                                                                                                                                                          Location/Qualifiers
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/function= promoter
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                                                                                                                                                                                                                                                                                                                                                  93DE-4306832.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 2; 8pp; German.
                                                                                                                                                                                                                                                                                                                                                                    93DE-4306832
                                                                                                                                   AAQ56057 standard; DNA; 31
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                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1994-058406/08.
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Matches 31; Conserv
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31 AGCCGCGGGGCTAGTATTACCCCCGCGGCT 1

AAX02688 standard; DNA; 31 BP

RESULT 15 AAX02688/c

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Stem loop; coconut foliar decay virus; CFDV; bacterial promoter;
yeast promoter; tissue-specific; phloem-specific; CaMV 35S promoter; ss.
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/*tag= c
/note= "Region binds to nucleotides 1 to 11"
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                                                                                                                        Location/Qualifiers
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Best Local Similarity
Matches 31; Conserv
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                                                                           Gemini virus
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  Stem loop;
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Page 10

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June 19, 2002, 16:09:16; Search time 247.21 Seconds (without alignments) 378.570 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                        383533 seqs, 122816752 residues
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381
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Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries Issued\_Patents\_NA:\* Database :

1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*
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6: /cgn2\_6/ptodata/1/ina/pcTUS\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARTES

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NON	Score	Match	Match Length DB	DB	ID	Description
,	1 291	76.4	1291	4	US-09-462-975-1	Sequence 1, Appli
O	2 32.2	8.5	4411529	4	US-09-103-840A-1	i
υ	3 31	8.1	31	4	US-09-462-975-2	$^{\circ}$
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1		7.2	1128	4	US-08-976-259-96	96
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7		7.2	1065	1	US-08-734-792-1	Ĥ
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121 cacaataaaagatteeatttggataagaacgaatetgttaetttgettgeagtgeacgea 180

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8 818-111-105 9-056-556-110 9-131-028A-8 9-131-028A-8 9-131-028A-6 9-131-028A-10 9-426-557-1 9-426-557-1 9-426-557-1 9-426-557-1 9-303-069-17 9-303-069-17 9-303-069-17 9-303-069-17 8-323-084A-7	SIA	DNA AS A PRO 462,975 18/04345 12.4 12.4 15ion 4.0 15ion 4.0 16 Artificial 18 17 Artificial 18 18 Artificial 18 18 Artificial 18 18 Artificial 18 18 Artificial 18	tato	aate 
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80 - Sn 60		TULT 1  19.462-975-1  Gquence 1, Application US/09462975  atent No. 6303345  APPLICANT: Rohde, Wolfgang APPLICANT: Rohde, Wolfgang APPLICANT: Randles, John W. APPLICANT: Balamin, Francesco CURRENT APPLICATION NUMBER: US/09/462,975  CURRENT FILING DATE: 1998-07-17  PRIOR APPLICATION NUMBER: PCT/EP98/04345  PRIOR APPLICATION NUMBER: 19730502.4  PRIOR FILING DATE: 1997-07-16  NUMBER OF SEQ ID NOS: 7  SOFTWARE: FastSEQ for Windows Version 4.0  LENGTH: 1291  TYPE: DNA  TYPE: DNA  TYPE: DNA  TYPE: DNA  TYPE: DNA  TYPE: DNA  TYPE: OTHER INFORMATION: CONSTRUCT  09-462-975-1  UBLY MATCH  TO SET LOCAL Similarity 100.0%; Pred. No. 1.1e  atches 291; Conservative 0; Mismatches	cgt       cgt	lagg       agg
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33 22777		SULT 1 Sequence 1, Application US/0946297 Sequence 1, Application US/0946297 GEREAL INFORMATION: APPLICANT: Rohde, Wolfgang APPLICANT: Readles, John W. APPLICANT: Becker, Dieter APPLICANT: Bandles, John W. APPLICANT: Salamini, Francesco TITLE OF INVENTION: USE OF VIRUS FILE REFERENCE: 23232.000311 CURRENT APPLICATION NUMBER: US/09 CURRENT FILING DATE: 1998-07-13 PRIOR FILING DATE: 1999-07-13 PRIOR FILING DATE: 1997-07-16 NUMBER OF SEQ ID NOS: 7 SSCHWARE: FastSEQ for Windows Ve SSCHWARE: PastSEQ for Windows Ve SSCHWARE: DNA ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: CONSTRUCT OTHER CONSTRUCT OTHER CONSTRUCT OTHER CONSTRUCT OTHER CONSTRUCT OTHER CONSTRUCT OTHER	Scca IIII	ctac tac
		pplicatio 103345 Randles, Wo Becker, D Becker, D Becker, D Becker, D Becker, D Salamini, CE: 2323 ICATION NUM DATE: 1 O ID NOS: CO ID NOS: CATION NUM DATE: 1 CO ID NOS: CATION NUM CATION NUM CATION NUM CATION NUM CATION ID NOS: CATION ID NOS: CATION ID NOS: CATION ID NOS: CATION ID NOS:	)           30000000000000000000000000000	gtg       gtgc
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US-08-289-222E-5
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APPLICANT: FRSER, Claire M.
APPLICANT: VERSER, Claire M.
APPLICANT: VENTER, JOHN C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
NUMBER OF SEO ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
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OTHER INFORMATION: construct
US-09-462-975-2
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                   241 ctatctaccgtccatttgtttttgcgcgatcggacggctgagttgatctgg 291
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APPLICANT: Randles, John W.
APPLICANT: Hehn, Alain
APPLICANT: Hehn, Alain
APPLICANT: Balamini, Francesco
TITLE OF INVENTION: USE OF VIRUS DNA AS A PROMOTER
FILE REFERENCE: 2323.200301
CURRENT FILING DATE: 2000-05-17
PRIOR APPLICATION NUMBER: US/09/462,975
PRIOR APPLICATION NUMBER: PCT/EP98/04345
PRIOR APPLICATION NUMBER: 19780502.4
PRIOR FILING DATE: 1998-07-13
PRIOR FILING DATE: 1997-07-16
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
                                                                                                                                                                 Sequence 1, Application US/09103840A Patent No. 6294328
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APPLICANT: FLEISCHMAN, Robert D.
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APPLICANT: Rohde, Wolfgang
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Matches 58; Conserv
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DB 4; Length 31;

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Query Match

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                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B TITLE OF INVENTION: FAMILY
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Pred. No. 0.14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/289,222E
FILING DATE: 25-AUG-1999
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: ED 92102324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 11-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: P564-9021
FELING DATE: 10-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: P564-9021
FERERBENCE/DOCKET NUMBER: P564-9021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NIKAIDO, MARMELSTEIN, MURRAY & ORAM
100.0%; Pred. No. 0.019;
:ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                    331 agccgcgggggctagtattacccccgcggct 361
                                                                                             31 AGCCGCGGGGCTAGTATTACCCCCGCGGCT 1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                       Sequence 5, Application US/08289222E Patent No. 6120760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: CDNA from mRNA US-08-289-222E-5
                                                                                                                                                                                                                                                                                  APPLICANT: HOTTEN, GERTRUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.9%;
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Best Local Similarity 59.39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGIH: 265 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                      31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 5: CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
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APPLICANT: HOTTEN,
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79 TGCCTCCTTTCACACTGCAGTGCTCA 104
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                                                                                                                                                                                                                                                                                                                                                                                                   2088
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19 CGCCATGAACTICTGCATAGGGCAGTGCCCACTACACATAGCAGGCATGCCTGGTATTGC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.9%; Score 30; DB 4; Length 265; 59.3%; Pred. No. 0.14;
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                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
STREET: SUITE 330
CITY: WASHINGTON
                                                                                                                                                                                                                         APPLICANT: H TTEM, GERTRUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
APPLICANT: POHL, JENS
TITLE OF INVENTION: DAS SEQUENCES ENCODING NOVEL
TITLE OF INVENTION: GROWTH/DIFFERENTATION FACTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFWHARE: Patentin Release #1.0, Version #1.25 SOFWHARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,526B FILING DATE: 03-APR-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: DE P 44 23 190.3 FILING DATE: 01-JUL-1994 PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 12-FEB-1993
ATTOKNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,105
REPERBENG-FOCKET NUMBER: P564-8005
TELECOMMUNICATION INFORMATION:
TELECHONE: 202/638-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 08/289,222 FILING DATE: 12-AUG-1994 PRIOR APPLICATION DATA:
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                                                         79 TGCCTCCTTTCACACTGCAGTGCTCA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                ; Sequence 5, Application US/09054526B
; Patent No. 6197550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: CDNA from mRNA US-09-054-5268-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 59.38
Marches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           265 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 202/638-4810 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'RY: USA
20005-5701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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APPLICANT: H TTEN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                         RESULT 5
US-09-054-526B-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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225 agaaagccgcaagcctctatctaccgtccatttgttttgcgcgatcggacggctgagtt 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.9%; Score 30; DB 4; Length 2088; Best Local Similarity 27.9%; Pred. No. 0.45; Matches 46; Conservative 36; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: zdint1 amino acid degenerate sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    285 gatotggcgccaaaacctctgctaagtcccgtgctaagtataaa 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY, AND ORAM STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY, STREET: SUITE 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 GNACNGCYTTRTTRTGYTTYTGYTGRTGNCKNGCYTTNGTRTCNA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: HOTTEN, GERTRUD
APPLICANT: HEIDHART, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: DOHL, JENS
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS
CORRESPONDENCES: 49
CORRESPONDENCE ADDRESS:
                                                                                                  GENERAL INFORMATION:
APPLICANT: Shepperd, Paul O.
APPLICANT: Shepperd, Nand
APPLICANT: Baindur, Theresa A.
APPLICANT: Bishop, Paul D.
TITLE OF INVENTION: DISINTEGRIN HOMOLOG
FILE REFERENCE: 98-29
CURRENT APPLICATION NUMBER: US/09/351,414
                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: variation
LOCATION: (1)...(2088)
OTHER INFORMATION: n is any nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08482577B Patent No. 5807713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1)...(2088)
; OTHER INFORMATION: n = A,T,C or G
US-09-351-414-3
RESULT 6
US-09-351-414-3/c
Sequence 3, Application US/09351414
; Patent No. 6265199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 13
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292 cgccaaaaacctctgctaagtcccgtgctaagtataaatagccgcggggggtagtattac 351
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APPLICANT: NEIDHARDT, HELGE
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BELFOLD, ROLF
APPLICANT: BOHL, JENS
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B
MINDER OF INVENTION: FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.9%; Score 30; DB 1; Length 227
59.3%; Pred. No. 0.47;
tive 0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
STREET: SUITE 330
STREET: WASHINGTON
STATE: WASHINGTON
                                                             PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                   APPLICAL.

FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, SHARON
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: 9564-5010
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TFILEPHONE: 202/638-4810
TFILEPAX: 202/638-4810
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07-JUL-1994
                                                        SOFTWARE: Patentin Release #1.0, VeCURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,577B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/289,222E
FILING DATE: 25-AUG-1999
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-A0G-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1000 IGCCICCTITCACACIGCAGIGCICA 1025
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                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                           TELEFAX: 202/638-4010
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
TRNGTH: 2272 base pairs
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 59.34
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 20005-5701
MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-482-577B-1
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GENERAL INFORMATION:

APPLICANT: H TTEN, GETTING
APPLICANT: H TTEN, GETTING
APPLICANT: NEIDHARDI, Helge
APPLICANT: POHL, Jens
APPLICANT: POHLESTA, Michael
TITLE OF INVENTION: TGF- FAMILY
NUMBER OF INVENTION: TGF- FAMILY
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 7.9%; Score 30; DB 3; Length 2272; Best Local Similarity 59.3%; Pred. No. 0.47; Matches 51; Conservative 0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
STREET: 655 Fifteenth Street, N. W., G Street Lobby,
STREET: Suite 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: EPO 92102324.8 FILING DATE: 12-FEB.1992
PRICRA PAPLICATION DATA: APPLICATION NUMBER: PCT/EP93/00350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UMBER: PCT/EP96/03065
12-JUL-1996
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FILING DATE: Herewith
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                                                                                  FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTE, MONICA CHIN
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-
TELECOMMUNICATION INFORMATION:
TELEFAX: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09218176 Patent No. 6171584
                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: CDNA from mRNA
US-08-289-222E-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 12-JUL-1996 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                 LENGTH: 2272 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
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APPLICATION NUMBER: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: APPLICATION NUMBER: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-218-176-1
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,222
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US-08-686-968C-228
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?: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
P. SUITE 330
WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09054526B
Patent No. 619750
GENERAL INFORMATION:
APPLICANT: H TTEN, GERTRUD
APPLICANT: HECHOLD, ROLF
APPLICANT: POHL, JENS
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
TITLE OF INVENTION: GROWTH/PDIFFERENTATION FACTORS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMERR: US/09/054,526B
FILING DATE: 03-APR-1998
                                                                                                                                            APPLICATION NUMBER: EP 92 102 324.8 FILING DATE: 12-FEB-1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: DF 94 23 190.3 FILING DATE: 01-JUL-1994 APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: DE 195 11 243.1 FILING DATE: 27 MAR-1995 ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                    TORNEY/AGENT INCOMENTAL NAME: KITTS, MONICA Chin REGISTRATION NUMBER: 36,105
                     APPLICATION NUMBER: PCT/EP93/00350 FILING DATE: 2-FEB-1993 PRIOR APPLICATION DATA:
                                                                      FILING DATE: 7-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1000 TGCCTCTTTCACACTGCAGTGCTCA 1025
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 202/638-4810 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 2272 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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ZIP: 20005-5701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE:
US-09-218-176-1
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APPLICANT: Cochran, Mark D.
APPLICANT: Cochran, Mark D.
APPLICANT: JUNKET, David E.
TITLE OF INVENTION: Recombinant Swinepox Virus
FILE REFERENCE: 39119-H/JML
CURRENT APPLICATION NUMBER: US/08/686,968C
CURRENT FILING DATE: 1996-07-25
NUMBER OF SEQ 1D NOS: 231
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
            PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 44 23 190.3

FILING DATE: 01-70L-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EPO 92102324.8

FILING DATE: 12-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP93/00350

FILING DATE: 12-FEB-1993

ATTORNEY/AGENT INFORMATION:

NAME: KITTS, MONICA CHIN

REGISTRATION NUMBER: 36,105
                                              DE P 44 23 190.3
                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-8005
TELECOMMUNICATION INFORMATION:
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Patent No. 6221361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: cDNA from mRNA
US-09-054-526B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.98;
                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 2:
FILING DATE: 12-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 2272 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.99
Best Local Similarity 59.39
Matches 51; Conservative
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Matches 54; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: CDS
; LOCATION: (1)..(1407)
US-08-686-968C-228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.3%; Score 27.8; DB 4; Length 3129; 51.2%; Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 96, Application US/08976259
Patent No. 6316609
GENERAL INFORMATION:
APPLICANT: Dillon, Patrick J.
APPLICANT: Choi, Gil H.
APPLICANT: Welch, Rodney A.
TITLE OF INVENTION: Nucleotide Sequence of Escherichia coli
Patent No. 6316609
NUMBER OF SEQUENCES: 142
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Sterne, Kessler, Goldstein & Fox P.L.L.C 1100 New York Ave, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US 60/031,626 AND US 60/061,953
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ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62;
                     158 ttactttgcttgcagtgcacgcaaccactttccac 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                     APPLICANT: Warren, Patrick V.
APPLICANT: Warren, Richard L.
TITLE OF INVENTION: dnaE
TITLE OF INVENTION: GNAE
CURRENT APPLICATION NUMBER: US/09/387,695
CURRENT FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,259
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Streptococcus pneumoniae US-09-387-695-1
                                                                                                                                       Sequence 1, Application US/09387695
Patent No. 6280990
                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: May, Earl
APPLICANT: Van Horn, Stephanie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2013 ggaaaaa 2019
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                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 3129
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                                                                                                 RESULT 12
US-09-387-695-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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132 attecatttggataagaaegaatetgttaetttgettgeagtgeaegeaaceaettteea 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BERGETOGEM, SVEN
APPLICANT: BERGETOGEM, SVEN
APPLICANT: HERNELL, OLLE
APPLICANT: LOENNERDAL, BO
APPLICANT: TOENNERDAL, BO
APPLICANT: TOENNERDAL, BO
APPLICANT: TOENNERL, JAN
APPLICANT: TOENNELL, JAN
APPLICANT: STRORMQLIST, MATS
TITLE OF INVENTION: HUMAN BETA-CASEIN PROCESS FOR PRODUCING
TITLE OF INVENTION: 1T AND USE THEREOF
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                   1488.0740002/EKS/CBM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: WO PCT/DK92/00236 FILING DATE: 19-AUG-1992 PRICATION DATA: APPLICATION NUMBER: WO PCT/DK91/00233 FILING DATE: 19-AUG-1991 ATTONNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/078,090 FILING DATE: 19930618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 cgtcaccaatccaggtgagtagcttg 217
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 24, Application US/08078090 Patent No. 5739407 GENERAL INFORMATION:
                NAME: Steffe, Eric K.
REGISTRATION UNUBER: 36,688
REFERNCE/DOCKET NUBER: 1488.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-250
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 1128 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BROWDY AND NEIMARK
ATTORNEY/AGENT INFORMATION:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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US-08-976-259-96
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28,005

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LOCATION:
IDENTIFICATION METHOD: DNA sequencing and restriction analysis
IDENTIFICATION: The encoded product of nucleotide SEQ ID NO: 1: is the hum
OTHER INFORMATION:
AUTHORS: B. Lonnerdal et al
TITLE: Cloning and Sequencing of a CDNA encoding human
TITLE: milk beta-casein.
JOURNAL: Federation European Biochemical Society Letters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 cccacgcgctatcgtttacatcttatgaatatcctgcccaggccgaaggcctgggaggtg 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 7.2%; Score 27.4; DB 1; Length 1065; Best Local Similarity 55.9%; Pred. No. 2.9; Matches 52; Conservative 0; Mismatches 41; Indels 0.
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TISSUE TYPE: Mammary Gland
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE: Human Mammary Gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Search completed: June 19, 2002, 16:22:15 Job time: 15793 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RELEVANT RESIDUES IN SEQ ID NO:
                  INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: Adult
                                                                                                                                                                                                                   CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153 - 156
1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                     LIBRARY:
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APPLICANT: MUKETI, P.
APPLICANT: SCO, A.
APPLICANT: SCALIER, J.
APPLICANT: Schaller, J.
TITLE OF INVENTION: Product for the Inhibition of Infection of Mammalian Cells by NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                              ;
0
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MEDIUM TYPE: 3.5 inch, 1.44 Mb storage (B)COMPUTER: Apple Macintosh OPERATING SYSTEM: MacIntosh System 7.1(D)SOFTWARE: ClarisWorks 1.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/249,554 ·
FILING DATE: 26-MAY-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA: No. 5506209 applicable
TELECOMMUNICATION DATA: No. 5506209 applicable
TELEFAN: (614) 624-3774
TELEFAN: (614) 624-3774
TELEFAN: (614) 624-3774
TELEFAN: (614) 624-3774
TELEFAN: (618) 624-3774
TELEFAN: (619) 00: 1:
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DESCRIPTION: Human milk 'eta-casein
                                                                                                                                                                                                                                                                                                                  7.2%; Score 27.4; DB 1; Length 708; 55.9%; Pred. No. 2.3; tive 0; Mismatches 41; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72 ctacccggccgaaggccgggaacaatatgaatc 104
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  BERGSTROM2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Lonnie R. Drayer
ADDRESSEE: ROSS Products Division
ADDRESSEE: Abbott Laboratories
STREET: 625 Cleveland Avenue
CITY: Columbus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08249554
Patent No. 5506209
REFERENCE/DOCKET NUMBER: BE TELECOMMUNICATION INFORMATION:
                                                                                                              24:
                                                                                  TELEX: 248633
INFORMATION FOR SEQ ID NO: 24
SEQUENCE CHARACTERISTICS:
LENGTH: 708 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                          TELEPHONE: (202)628-5197
TELEFAX: (202)737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1065 base pairs
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Best Local Similarity 55.9%
Matches 52; Conservative
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STRANDEDNESS: Single
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FRAGMENT TYPE:
ORIGINAL SOURCE: Human
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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on:

June 19, 2002, 14:04:23; Search time 7489.97 Seconds

(without alignments)
686.563 Million cell updates/sec

Title:

VS-09-462-955B-1_COPY_611_991

Perfect score:

Jatacccgcccacgcgc........ccccaacctctgctaacccc 381

Scoring table:

Gapop 10.0, Gapext 1.0

Searched:

J3336207 Seqs, 6748477542 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum Match 08
Maximum Match 1008

Listing first 45 summaries
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1: em\_estba:\*
2: em\_esthum:\*
3: em\_esthum:\*
4: em\_esthum:\*
5: em\_estov:\*
6: em\_estov:\*
7: em\_estro:\*
8: em\_ltc:\*
9: gb\_est:\*
10: gb\_est2:\*
11: gb\_ltc:\*
12: gb\_gst:\*
13: em\_gss\_hum:\*
14: em\_gss\_hum:\*
15: em\_gss\_vrt:\*
16: em\_gss\_vrt:\*

EST: \*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

0.00	Desci Thrion	BH175883 004 P 17-	AL612823 T3 end of	AL667528 AL667528	AL067144 Drosophil	BG006561 OV4-GN014	AI065300 TENU2187	BB610652 BB610652	AZ339575 1M0071B12	AV763886 AV763886	AQ459250 HS_5078_A	BH437599 BOHAW63TF	AA221432 my22e11.r	D61210 HUM168A07B	AI910101 RC-BT236-	AL084760 Arabidops	B30289 F9H2TF IGF	BI011057 QV2-EN009
SUMMARIES		BH175883	CNS07IRP	AL667528	CNSOODBS	BG006561	AI065300	BB610652	AZ339575	AV763886	AQ459250	BH437599	AA221432	D61210	A1910101	CNSOOPOA	B30289	BI011057
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Score		35	35	34.4	34	33.6	33.4	33.2	33	33	33	32.8	32.6	32.4	32.4	32.4	32.4	32.4
Result No.		1	5	e	ပ •	2	9	c 2	ထ	6	10	c 11	12	13	14	15	16	17

	AG145147 Pan trogl	AL106603 Drosophil	AL259384 Tetraodon	AK010602 Mus muscu	AI053376 TENU1541	AI026415 TENU0626	BM489876 pqm2n.pk0	AW450316 UÎ-H-BIĴ-	AI974978 EST269572	C79787 C79787 Mous	BE246832 TCBAP1E51	AI205836 qq33f11.x	AA834925 aj39a02.s	AQ012189 327P1E067	AI016082 ov26q10.x	AA889602 ak28d03.s	BB295841 BB295841	BB285126 BB285126	AW037599 EST279057	BH087127 RPCI-24-3	AZ564822 201PvH06	BF234647 602028464	AW014292 UI-H-BIO-	BH540957 BOGY029TR	AQ874985 V119G9 mT	AG145182 Pan troql	
CNS010B7	AG145147	CNS016DD	CNS03T4V	AK010602		ď		AW450316				K	AA834925		Æ		BB295841		AW037599	BH087127	AZ564822	BF234647	AW014292	BH540957	AQ874985	AG145182	BH451673
787 12	1153 12	201 12	037 12	210 11				533 9									297 9				636 12		298 9	• •	625 12		694 12
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32.4	32.4	32.4	32	32	31.8	31.8	31.8	31.8	31.8	31.8	31.6	31.6	31.6	31.6	31.4	31.4	31.2	31,2	31.2	31.2	31.2	31.2	31	31	31	31	31
18	c 19	20	21	22		c 24	c 25	26	c 27	c 28	c 29	30	31	c 32	33	34	c 32	c 36	37	38	39	40	41	42	43	C 44	c 45

## ALIGNMENTS

BH175883 524 bp DNA linear GSS 29-OCT-2001 004_P_17-rev SmBAC1 Schistosoma mansoni genomic clone 004P17 5', DNA sequence.	BH175883.1 GI:16274497 GSS. Schistosoma mansoni. Schistosoma mansoni platyhelminthes; Trematoda; Digenea; Bukaryota; Metkazoa; Platyhelminthes; Schistosomai idae: Schistosoma.	1 (bases 1 to 524) Le Paslier, MC., Pierce, R.J., Merlin, F., Hirai, H., Wu, W., Williams, D.L., Johnston, D., LoVerde, P.T. and Le Paslier, D. Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library Genomics 65 (2), 87-94 (2000)	20247247 Other_GSSs: 004_P_17-21 Contact: Pierce RJ INSERW 167 Institut Pasteur de Lille I rue du Professeur A. Calmette, 59019-Lille, France Fax: (33) (0)3 20877783 Fax: (33) (0)3 2087788 Emall: Raymond.Pierce@pasteur-lille.fr	Cass sequencing 12-20cAnOverHOPEL bases 1-130 may 60s lucitly to S.mansoni EST A1974978.1 from base 292-163. Bases 283-408 have 84% identity to S.mansoni EST A1394783.1 from base 448-326. Plate: 004 row: P column: 17 Seq primer: M13 reverse primer Class: BAC ends High quality sequence stop: 524.  Location/Qualifiers 1524 //organism="Schistosoma mansoni" / strain="Puerto-Rican" / strain="Puerto-Rican" / clone="004P17" / clone="004P17"
RESULT 1 BH175883 LOCUS DEFINITION	VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL	MEDLINE COMMENT	FEATURES

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Best Local Similarity
                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSS 08-OCT-2001
                                      /dev_stage="cercariae"
//dab_host="bloomphalaria glabrata" //hab_host="bloomphalaria glabrata" //hab_host="bloomphalaria glabrata" //hab_host="bloomphalaria listel" in digested and size-selected S. mansoni cercarial DNA was ligated anno Hind III digested placeont on the digested placeont on the digested placeont on the complete library contains 23808 clones from 4 independent sizing-ligation-transformations. Average insert size sizing-ligation-transformations. Average insert size anges from 70-17 kb and genome coverage is 7.9-fold."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNSO7IRP 524 bp DNA linear GSS 08-OCT-2001
T3 end of clone 004CH09 of library SmBAC1 from strain Puerto-Rican
of Schistosoma mansoni, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeldida; Schistosomatoidea; Schistosomatidae; Schistosoma. 1 (basea 1 to 524)
Le Paslier, M.C., Pierce, R.J., Merlin, F., Hirai, H., Wu, W., Williams, D.L., Johnston, D., Loverde, P. T. and Le Paslier, D. Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library
                                                                                                                                                                                                                                                                                                                                                                                                            59 AGNTACTICGGATCCGTTGGCCAGACACTATCAGCAACAAGCTAGTGTGGGACWWAACAA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 ACCANATTCCAGTTGGAGGAAAAATCACAGANNYRYTBCTGGAAGTGGATANGACACAC 178
                                                                                                                                                                                                                                                                                                                         9.2%; Score 35; DB 12; Length 524; 50.0%; Pred. No. 1.1;
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/strain="Puerto-Rican"
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                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
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/clone="004CH09"
/clone_lib="SmBAC1"
/note="end : T3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomics 65 (2), 87-94 (2000)
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/clone_lib="SmBAC1"
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Schistosoma mansoni
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CNSOODBS 1101 bp DNA linear GSS 04-JUN-1999 Drosophila melanogaster genome survey sequence T7 end of BAC # BACR27J14 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                     AL667528 directional larval cDNA library Ciona intestinalis cDNA clone 0202G05 5', mRNA sequence.
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Phlebobranchia; Cionidae; Ciona.
1 (bases 1 to 898)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 gcagtgcacgcaaccactttccacgtcaccaatccaggtgagtagcttgctggagaagaa 228
                                                                            59 AGNTACTICGGAICCGTIGGCCAGACACTAICAGCAACAAGCIAGIGIGGGACWWAACAA 118
                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 GTAATACATGAACAACATTCCACGTCACCAAACGTTGTGAGTATATTGCTTGTGCAATG 357
                                       0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:7719"
/clone="0202605"
/clone_lib="directional larval cDNA library"
   Length 524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ciona intestinalis directional larval cDNA library
Unpublished (2002)
Contact: Genoscope
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                                       65;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pBluescript2SK+"
186 c 157 g 265 t
Score 35; DB 12;
Pred. No. 1.1;
4; Mismatches 65,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Ciona intestinalis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229 agccgcaagcctctatctaccgtccatttgtt 260
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 9.2%;
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                                                                                                                                                                                                                                                                   179 TTTCMGGAAATCCCCCCA 196
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Ciona intestinalis
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                                         69; Conservative
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/dev_stage="Adult"
/dev_stage="Adult"
/note="Organ: placenta_normal; Vector: puc18; Site_1: Smal; Site_2: Smal; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
                                                                                                                                                                                                                                                          Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/soripts/gethtml2.pl?tl=QV4.t2-QV4-GN0143-
271100-579-c076t3=2000-11-276t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 260.
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                                                                                                          Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91 gaacaatatgaatcgagttatggggggggcccacaataaaagattccatttggataagaac 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 gaatctgttactttgcttgcagtgcacgcaaccactttccacgtcaccaatccaggtgag 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 atcttatgaatatcctgcccaggccgaaggcctgggaggtgctacccggccgaaggccgg 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        193 ACCTCGTGATCCGCCTGCCTCGCCTCCCCACAGTGCTGAGCTTACCGCTTTACGTCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             253 GGACACTGAACATTTACTTTGGCTGATCCTCATGAACCGTGCTTTTAGCACGAC
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
                        Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
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                                                                                       Contact: Simpson A.J.G
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                                                                                                                                                                                                                 Tel: +55-11-2704922
                                                                                                                                                                                                                                          Fax: +55-11-2707001
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                                                                                                                                                                                                                                                                                                                                                       Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosphila Genome Project (BDGP).
The BDGP is constructing a physical map of the prosophila melanogaster genome using these BACs. For further information pleases see http://www.fruitfly.org The BDGP Drosphila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Magal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, C.S., Simpson, D.H., Brunstein, A., de Gollveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG006561 403 bp mRNA linear EST 24-JAN-2001 QV4-CN0143-271100-579-c07 GN0143 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 403)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shorgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 tttccacgtcaccaatccaggtgagtagcttgctggagaagaaagccgcaagcctctatc 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1043 YAAACGGSCCBTKWRABATAWAAACAAAWTTTTTWTTTWGWTTTTTGTGCWAATMACAYC 984
                                                                                                                                                        Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Ptertygota: Neoptera: Endopterygota; Diptera; Brachycera;
Muscomorpha: Ephydroidea; Drosophilidae; Drosophila.
( Pases 1 to 1101)
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11.7%; Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="RPCI-98"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23; Mismatches
genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                                                                                                          Drosophila melanogaster
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                                                 AL067144.1 GI:4947840
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1711 (2000)

IO (11), 1757-1771 (2000)

Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
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Yamanaka,I., Kiyosawa,H., Kondo,S., Saito,T., Shinagawa,A., Aizawa,K., Tehukda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K., Arakawa,T., Ishi,Y. and Hayashizaki,Y.
Ishii,Y. and Hayashizaki,Y.
Func. Genomics 2 pre, L72-186 (2001
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Site_1: XhoI; Site_2: SstI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5" GAGAGAGAGCGTCTTTTTTTTTTTTTTTTTVN 3"], CDNA was
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
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51.6%; Pred. No. 6;
Ive 0; Mismatches 33; Indels 0;
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/dev_stage="adult"
/lab_host="SOLR"
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Best Local Similarity 61.6%;
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BB610652 RIKEN full-length enriched, adult male tongue Mus musculus
cDNA clone 2310065E04 5', mRNA sequence.
BB610652
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1030)
Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A.
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URL:http://genome.gsc.riken.go.jp/
Carninci, P., Shibata,Y., Hayetsu,M., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
,prepare full-length cDNA libraries for rapid discovery of new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="T. cruzi epimastigote normalized cDNA Library"
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The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
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/note="cDNA library constructed with oligo dr primed
/note="cDNA library constructed with oligo dr primed
epimastigote mRNA and cloned in pt7t318D phagemid with
modified polylinker (PHARMACIA)
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                                                                                                     Uppsala University
Biomedical Center, Box 589, S-751 23 Uppsala, Sweden
Tel: 46 18 471 45
Fax: 46 18 52 68 49
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                                                                                                                                                                                                                                                                                                                                                          /organism="Trypanosoma cruzi"
/strain="Cl-Brenner"
/db_xref="taxon:5693"
/clone="18e16"
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                                                                                                                                                                                                                  Email: lena.aslund@medgen.uu.se
Seq primer: T7
High quality sequence stop: 284.
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Contact: Yoshihide Hayashizaki
                                                                              Department of Medical Genetics
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Contact: Aslund L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.5 Kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gil47321141gblAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to
                                                                                                                                                                                                                                                                                \rm Rm.~308 , Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adaptored vector DNA, and transformed into chemically-competent E. coll XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
186 c 100 g 181 t
                   1 (bases 1 to 644)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A.
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. Coli strain XLIO-Gold, T1-resistant, F-"/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AV763886 MDS Homo sapiens cDNA clone MDSEEE03 5', mRNA sequence.
AV763886
                                                                                                                                  Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 ttactttgcttgcagtgcacgcaaccactttccacgtcaccaatccaggtgagtagcttg 217 | | | | | | | | | | | | | | | | | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354 TITCTGTGCACTGAGTGTAGGTTATCTCTGTCCTTACAAGCCTAAGGCATTCTCTGG 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="UUGC1M0071B12"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 8.7%; Score 33; DB 12; Length 644; 11 Similarity 60.7%; Pred. No. 5.6; 54; Conservative 0; Mismatches 35; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                      Std Error: 0.00
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Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
                                                                                                                                                                                     Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High quality sequence stop: 644.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 ctggagaagaaagccgcaagcctctatct 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              294 CITTAATAAAGAGCTGCAAGCCTATATCT 266
                                                                                                                                                                                                                                                                                                                                                                             Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="C57BL/6J"
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                                                                                                                and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Class: plasmid ends
                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
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                                              AUTHORS
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Homo sapiens

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 762)

Gu,J., Zhao,M., Huang,O., Xu,X., Li,Y., Peng,Y., Song,H., Xiao,H.,

Gu,Y., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,Y., Gao,G., Zhang,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G.,

Yang,Y., Gao,G., Zhang,O., Chen,S., Han,Z. and Chen,Z.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 977)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                   Contact: Zegung Han Cenome Center at Shanghai Schinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919(ex.45) Fax: 86-21-508019122 Email: hanzgechgc.sh.cn This clone is available at CHGC in Shanghai.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pTriplEx2; Site_1: sfiIA; Site_2: sfiIB" 172 c 177 g 209 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="Bone marrow"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 catttggataagaacgaatctgttactttgcttgcagtgcacgcaaccactttccacgtc 195
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48.9%; Pred. No. 6.1;
tive 0; Mismatches 91; Indels
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High Throughput Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MDSEEE03"
/clone_lib="MDS"
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AQ459250.1 GI:4637890
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Matches 87; Conservative
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Waterston, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pBACe3.6; Site_1: ECORI; Site_2: ECORI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and ECORI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at ECORI sites"
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Brassica oleracea
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 668)
Tromn, C.D., Van Aken, S., Utterback, T. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
Unpublished (2001)
                                                                                      Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 654 row: O column: 5
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BOHAW63TF BOHA Brassica oleracea genomic clone BOHAW63, DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TF
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/clone="plate=664 Col=5 Row=O"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
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             401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 others
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0; Mismatches
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Location/Qualifiers
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University of Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223 c
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Matches 54; Conservative
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Fax: 301-838-0208
                                                                                                                                                                                                                                                                             Class: BAC ends
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Location/Qualifiers

source

FEATURES

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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukarmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 659)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA221432 659 bp mRNA linear EST 13-FEB-1997 my22ell.rl Barstead mouse pooled organs MPLRB4 Mus musculus cDNA clone IMAGE:696620 5' similar to qb:L23769 Mouse microfibril-associated glycoprotein (MOUSE);, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                123 caataaaagatteeatttggataagaacgaatetgttaetttgettgeagtgeacgeaac 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183 cactttecacgteaceaatecaggtgagtagettgetggagaagaageageegeaageetet 242
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/clone="IMAGE:696620"
/clone_lib="Barstead mouse pooled organs MPLRB4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                   Length 668;
                                                                                                                                                                                                                                                                                                                                  67; Indels
                                                                                                                                                                                                                                                                              Score 32.8; DB 12;
Pred. No. 6.7;
0; Mismatches 67;
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/dev_stage="7 day"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 atctaccgtccatttgtttt 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /sex="mixed"
                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 52.19
Matches 73; Conservative
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AI910101.1 GI:6500781
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Best Local Similarity 55.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: +55-11-2704922
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Clontech human fetal brain polyA+ mRNA (#6535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 306)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Otsuka Pharmaceutical Co.,Ltd
463-10 kagasuno Kawauchi-cho, Tokushima, Tokushima, 771-01 Japan
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                                                                                                                                                                                                                                                 169 gcagtgcacgcaaccactttccacgtcaccaatccaggtgagtagcttgctggagaagaa 228
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ilarity 55.3%; Pred. No. 6.4;
Conservative 0; Mismatches 51;
                                                                                                                                                                                Score 32.6; DB 9;
Pred. No. 7.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Otsuka GEN Research Institute
                                                                                                                                                                                                                                                                                                             229 agccgcaagcctctatctaccgtccat 255
                                                                                                                                                                                                                                                                                                                                             83 AGCCGCCTGCCTCTTCCTGCTGTTCAT 109
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1. .306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fujiwara et al. (1995)
Unpublished (1995)
Contact: Tsutomu Fujiwara
                                                                                                                                                                                 8.6%;
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                                                                                                                                                                                               Local Similarity 60.9
es 53; Conservative
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Fax: 0886-37-1035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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Best Local Similarity
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Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?tl=RC&t2=RC-BT236-023.html
&t3=280499&t4=1)
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/hote="Organ: breast; Vector: pucl8; Site_1: SmaI, Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196
EST 30-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                              Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 359)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
                                                                                                                                                                                                                                                                                                                                                         Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsuklum,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNSOOPOA 414 bp DNA linear GSS 28-JUN-199
Arabidopsis thaliana genome survey sequence T7 end of BAC F9H2 of
IGF library from strain Columbia of Arabidopsis thaliana, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shorgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194 cccassascerrecceargreerrsecrescanarrsecrescarsecgersass 253
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                                 RC-BT236-280499-023 BT236 Homo sapiens cDNA, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gggaggtgctacccggccgaaggccgggaacaatatgaatcgagttatgggcgg 117
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359 bp
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/clone_lib="BT236"
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C bases 1 to 414)

Genoscope.

Direct Submission

Submitted (25-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr

Web : www.genoscope.cns.fr)

Location/Qualifiers
                                   Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases I to 414)
Salanoubat,M., Choisne,N., Artiguenave,F., Brottier,P., Wincker,P., Unpublished
                                                                                                                                                                                                                                                                                                                                                            /organism="Arabidopsis thaliana"
/strain="Columbia"
/db_ref="taxon:3702"
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/note="end : T7"
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Search completed: June 19, 2002, 14:04:28 Job time: 7526 sec

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Gaps

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95 aatatgaatcgagttatgggcgggcccacaataaaagattccatttggataagaacgaat 154

Query Match

8.5%; Score 32.4; DB 12; Length 414;
Best Local Similarity 60.0%; Pred. No. 7.3;
Matches 54; Conservative 0; Mismatches 36; Indels 0;

25 AATATGAATAAAGTTTTGATACACTTGAAATTAAAATATTCCAAAAGCGTGTTAACTAAT 84

155 ctgttactttgcttgcagtgcacgcaacca 184 

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PAT 17-DEC-2001
        AL442127 Human DNA
AC090043 Homo sapi
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1 (bass 1 to 1291)
Rohde, W., Becker, D., Randles, J.W., Hehn, A. and Salamini, F. Use of a virus DNA as promoter
Patent: US 6303345-A 1 16-OCT-2001;
Location/Qualifiers
                                                     AF269928
AX145246
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Sequence 1 from patent US 6303345.
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                                                       June 19, 2002, 15:48:13; Search time 5904.86 Seconds (without alignments) 995.850 Million cell updates/sec
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Copyright (c) 1993 - 2000 Compugen Ltd.
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DPKRNLILDVPRCNLEYLNYALLECVKNRAFSSDKYEPLSYLGFDHVHVLVFANVLPD
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TRPGVKRPRLAQRFAEEPDELRLEDPGGYRRCVVHGASVEWTRWAAENPFPFPYHNWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                         circular; complete genome.
Coconut foliar decay virus DNA, clones NMORG, pORG, and pORGSAU3A.
Coconut foliar decay virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; ssDNA viruses; Nanovirus.

1 (bases 1 to 1291)
Rohde,W., Randles,J.W., Langridge,P. and Hanold,D.
Nucleotide sequence of a circular single-stranded DNA associated with coconut foliar decay virus
Virology 176, 648-651 (1990)
                                                      1161 CTTTGCTTGCAGGCACGCAACCACTTTCCACGTCACCAATCCAGGTGAGTAGCTTGCTG 1220
                                                                                                                                                                                            61 ctttgcttgcagtgcacgcaaccactttccacgtcaccaatccaggtgagtagcttgctg 120
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                                    1 aatcgagttatggggcgggcccacaataaaagattccatttggataagaacgaatctgtta 60
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     Indels
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/db_xref="G1:323310"
/translation="MRTRRRREVRVCQISRTQARLVLHMWWNQKGRIVPVHRGPKTK
                                                                                                                                                                              /codon_start=1
protein_id="aAA42898.1"
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/translation="MTHTLNIPQFYSVPADFQIIRQDIGKYEYMHMVEPKITKGFVFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAA42899.1"
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/translation="MNRVMGGPTIKDSIWIRTNLLLCLQCTQPLSTSPIQVSSLLEKK
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This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known
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Human DNA sequence from clone RPI1-29716 on chromosome 13, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (26-3MN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
on Jan 28, 2001 this sequence version replaced gi:12578234.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 210115)
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16034. 16726

Anote="MLT1:INTERNAL repeat: matches 42. .880 of consensus"

Anote="MLT1D repeat: matches 40. .482 of consensus"

19077. .19259
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25657. .25831
/note="Charlie5 repeat: matches 2373. .2585 of consensus"
numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 http://www.sanger.ac.uk/HGP/Chrl3 RPI1-297I6 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                              This sequence is the entire insert of clone RPI1-29716 The true left end of clone RPI1-207010 is at 130589 in this sequence. The true right end of clone RPI1-272L14 is at 88495 in this sequence. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="MMR20 repeat: matches 7. .218 of consensus" 12023. .12404
/note="MMS20 repeat: matches 1. .394 of consensus" 1301. .14196
/note="MJ1V repeat: matches 1. .302 of consensus" 15743. .16019
/note="MLT1D repeat: matches 190. .505 of consensus" /note="MLT1D repeat: matches 190. .505 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .1650 of consensus"
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/note="L2 repeat: matches 2672. .2749 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="L2 repeat: matches 2335, .2504 of consensus" 2751. .20050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="Alusg repeat: matches 1. .302 of consensus"
20222. .20521
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29414. .29579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2363. .2502 More at 77% conserved" Anote-"70 copies 2 mer at 77% conserved" 3453. .3755 More-"Alur repeat: matches 1. .303 of consensus"
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/note="AluY repeat: matches 1. .311 of consensus"
28333. .28578
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28668. .28789
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5939. .5978

700te="10 copies 4 mer tgga 100% conserved"

9204. .9248
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/note="9 copies 4 mer acac 100% conserved"
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/note="15 copies 3 mer gtt 75% conserved"
10198. .10397
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/note="AluSc repeat: matches 1.5939. 5978
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30170. .30368
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29712. .29855
                                                                                                                                                                                                                                                               http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="13"
/clone="RP11-29716"
/clone="RP11-29716"
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/note="Sequence from overlapping clone bA272L14 (AL138689). Assembly confirmed by restriction digest."
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             /note="L1ME2 repeat: matches 6058. .6131 of consensus"
                                                                                                                                                                                                                                                                             /note="MIR repeat: matches 15. 257 of consensus" 34151. .34515
/note="LIN4 repeat: matches 4316. .4702 of consensus" 34520. .34746
/note="MIN1 repeat: matches 143. .365 of consensus" 34756. .34890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34891. .35118 / Anteres 162. .365 of consensus." /note="MLT1A1 repeat: matches 133. .365 of consensus." /note="MLT1A1 repeat: matches 133. .365 of consensus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MER92B repeat: matches 147. .626 of consensus" 39732. .40157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="THEIC repeat: matches 1. .426 of consensus" 40158. .40295
/note="MER92B repeat: matches 1. .148 of consensus" 40338. .42198
/note="LiMcD repeat: matches 115. .2032 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MLTIC repeat: matches 1. .497 of consensus" 44101. .44184
/note="MLTIH repeat: matches 448. .531 of consensus" 44362 .44400
/note="MLTIH repeat: matches 231. .269 of consensus" 44516 .44571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="MLT1J repeat: matches 300. .497 of consensus"
18579. .49021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MLTIC repeat: matches 264. .466 of consensus"
3715. .37003
/note="AluSg1 repeat: matches 1. .289 of consensus"
37056. .37085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .187 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MLT1A1 repeat: matches 63. .138 of consensus"
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45161. .45458
/note="AluSg repeat: matches 1. .298 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="MLT1A1 repeat: matches 1. .117 of consensus" 36404. .36604
                                                                                                                                                                                                                                                                                                                                                                                                                     /note="MLT1A1 repeat: matches 3. .138 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.70fe="15 copies 2 mer aa 93% conserved"
37616. 37989
Anote="THEIC repeat: matches 1. 371 of consensus"
3265. 39720
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50098. .51657
/note="THEIC-internal repeat: matches 1. .1580 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="MSTC repeat: matches 1. .405 of consensus"
                                                                                                                                                                                                                                       /note="MIR repeat: matches 85. .148 of consensus" 33747. .33968
                                                                                                      32558. .32703 // Note="73 copies 2 mer cc 63% conserved" 32623. .32754
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/note="MER5A repeat: matches 146.
42996. .43434
                                                         /note="CpG island"
/evidence=not_experimental
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                                         . .33462
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                                                                                                                                                                                         (AL138689)
33621. .330
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IAU86144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACU90043 173848 bp DNA linear PRI 11-FEB-2001
Homo saplens chromosome 3 clone RP11-551L4 map 3p, complete
sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 161323 CCAAGGTAGGTGATTATGTGAGGTAGGAATTTAACCCCCATGAGGCATATTCACACAAATT 161382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 161383 TGTTCACACCGGCTTGTGTGGTTGACTTCCTGTTACTCCAGAAACCACTTATAAAGCCACA 161442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 173848)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57276. .57714
/note="TIGGER2 repeat: matches 2268. .2718 of consensus"
                                                                                                                                  /note="MER53 repeat: matches 4. .189 of consensus" 53883. .54064
/note="LIM4 repeat: matches 5213. .5403 of consensus" 54288. .54498 repeat: matches 2146. .2357 of consensus" 55170. .55244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 tgtttttgcgcgatcggacggctgagttgatctggcgccaaaaacctctgctaagtcccg 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57716. .58679
force="L2 repeat: matches 1725. .2750 of consensus"
59166. .59480
                                                                           /note="MER31B repeat: matches 1. .477 of consensus" 53397. .53598
                                                                                                                                                                                                                                                                                                                   'note="HAL1 repeat: matches 657. .731 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="TIGGER2 repeat: matches 2. .65 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                       note="Alusc repeat: matches 5, .308 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              56584. .57221
/note="L2 repeat: matches 951. .1725 of consensus"
                        'note="THE1C repeat: matches 1. .371 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 161443 TGCGTAACATCTTTAACCAAAGTGCCAGGCTTTCACCCTGCTGTCATCGCACC 161495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           217 tgctaagtataaatagccgcgggggctagtattaccccgcgggctccccaacc 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.2%; Score 37; DB 9; Length 210115; 50.9%; Pred. No. 0.84; Live 0; Mismatches 85; Indels 0.
                                                                                                                                                                                                                                                                                                                         55482. .55663
/note="91 copies 2 mer tt 56% conserved"
55670. .55969
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Unpublished
                                                .52679
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AC090043.1 GI:12745081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 50.99
Matches 88; Conservative
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Influenza A virus (A/Swine/Quebec/192/81 (SwQc81)) neuraminidase mmRNA, complete cds.
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influenza A virus (A/Swine/Quebec/192/81 (SwQc81))
Viruses; SSRNA negative-strand viruses; Orthomyxoviridae; Influenza
virus A and B group; Influenza A viruses; Influenza A virus;
                                                          Submitted (11-FEB-2001) Human Genomic Center, Institute of Genetics, Chinese Academy of Sciences, Datun Road, Beijing, Beijing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db 126782 TICCATGIGAGGACTIGIGAAGAAGCCAGCAGAGACATICICAAICCTICTITITITIT 126841
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Arora,D.J.S., Tijssen,P., Dea,S. and Henrichon,M.
Complete sequences of the neuraminidase genes of swine influenza viruses (HINI) associated with the respiratory disease in pigs Virus Genes (1997) in press
2 (bases 1 to 1438)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 173848;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality coverage: 1.35x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              56; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: pUCl8; 100% of reads
Chemistry: Dye-terminator: ET 55% of reads
Chemistry: Dye-terminator Big Dye; 45% of reads
Assembly program: Phrap; version 0.990329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Consensus quality: 501 bases at least Q40 Consensus quality: 829 bases at least Q30 Consensus quality: 1046 bases at least Q20 Insert size: 1157; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 55.6%; Pred. No. 1.3;
Matches 70; Conservative 0; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="RP11-551L4"
56663 a 31451 c 31882 g 53852 t
                                                                                                                                                                                                                                                                                                                      Center project information
Center project name:1% project
Center clone name: RP11-551L4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                      Website:http://hgc.igtp.ac.cn
http://www.genomics.org.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                   ----Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /chromosome="3"
                                                                                                                                                                                                                                                                                                 Contact: hgc@igtp.ac.cn
                                                                                                                                                                            Center: Beijing Center
Center code: Beijing
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                                                                                                                    100101, P.R.China
Yu,J. and Yang,H. Direct Submission
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HPEVCNQSVVTYENNTWVNQTYVNISNTNIAAGOGVTPIILAANSPLCPISGRAIYSK
DNSIRIGSKGDIFVMREPFISCSHFECRTFFLTQGALLNDRHSNGTVKDRSPYRTLMS
CPIGEARSPYNSRFESYAWSAASACHDGMGWIJIGTSGPDNGAYAVLKYNGIITDTIKS
WRNKILRYGSSECVCINGSCFTIMTDGPSNGQASYKIFKMEKGKIIKSIELDAPNYHY
EECSCYPDTGKYVCVCRDNWTASNRRWYSFDONLDYQIGYICSGVFGDNPRSNGKGD
CGPVLSNGANGVKGFSFRYGNGVWIGRTKSISSRSGFEMIWDPSGWTETDSSFSMKOD
IIALTDWSGYSGSFVQHPELTGMNCIRPCFWVELIRGQPKESTIWTSGSSISFCGVNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MNTNQRIITIGTICLIVGIVSLLLQIGNIVSLWISHSIQTGEKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 29176)
Kaneko,T., Kato,T., Sato,S., Nakamura,Y., Asamizu,E. and Tabata,S.
Direct Submission
                        Submitted (21-JAN-1997) CRV, Institut Armand-Frappier, 531 Boul.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui Pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          737 CAAGCAATGGGCAGGCCTCGTACAAATATTCAAAATGGAGAAAGGGAAGATATTAAAAT 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (01-MAR-2000) Yasukazu Nakamura, Kazusa DNA Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Institute, Department of Plant Gene Research; 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp,
Tel:81-438-52-3935, Fax:81-438-52-3934)
                                                                                                                        /organism="influenza A virus (A/Swine/Quebec/192/81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
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Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches 35; Indels
                                                                                                                                                                     /strain="A/Sw/Quebec/192/81 (SwQc81)"
                                                                                                                                                                                        /db_xref="taxon:57280"
/note="tissue culture-adapted virus"
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                                                 des Prairies, Laval, QC H7N4Z3, Canada
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          386 t
                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="AAD00583.1"
/db_xref="G1:4099319"
                                                                                                                                                                                                                                                                                                                                /note="H1N1; peplomeric"
                                                                                                                                                                                                                                                                                                                                                                                   /product="neuraminidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      797 CGATTGAACTGGATGCACCTAATTACCAC 825
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60.7%;
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                                                                                                                                              (SwQc81))"
                                                                                                                                                                                                                                                                                                              /gene="NA"
                                                                                                  .1438
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                                                                                                                                                                                                                                          .1438
                                                                                                                                                                                                                                                                                      1. .1410
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20363099
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.17648,17753. .17930,18013. .18545,
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/note="gene_id:MYF5.1"
                        http://www.kazusa.or.jp/kaos/cgi-bin/add_graph.cgi?c=MTF5
Genes with similarity to proteins in the databases are described in
'product' or 'note 'qualifiers. Genes that have no significant
product' or 'note 'qualifiers. Genes that have no significant
protein similarity are described as 'unknown protein'.

The software programs used to predict genes include: Grail
(Informatics Group, Oak Ridge National Laboratory,
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),
NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://gremlinl.zool.iastate.edu/cgi-bin/sp.cgi).
                                                                                                                                                                                                                                                                                                                                                                                                                                         Genes encoding tRNAs are predicted by tRNAscan_SE (Seam Eddy, Washington University School of Medicine, St. Louis, http://genome.wustl.edu/eddy/tRNAscan_SE).
This sequence may not be the entire insert of this clone. It may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEVVDTTFEKEEGFKGGSSCYTALVSEGSLYVSNAGDCRAVMSVGEMMNGKELKPRED
MLICFTLWRIQGSLVVPRGIGDAQLKKWVIAEPETKISRVEHDHEFLILASHGLWDKV
SNOEAVDIARPFCLRTEKPLLLAACKKLVDLSASRGSFDDISVMLIPLRPVRIEKRGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="BAB01931.1"
/db_xref="G1:9294079"
/translation="MEDRFSTITNLHGDRKQAIFGVYVGHGGVKAAECPAKNLDKNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RLLKSDEIFKVRRERGVVEPSVFMLSSGDTCWTWFDKGFGNCQKLPELPSDICFLHGD
KESLCAGTHLIVTGKEEKSIALMYELETSKWFKGPAMITRATLFASATCGTVVFVAG
GLKIEGNGTHLIVTGKEEKSIALMYELLRGMHFKRFKGFGCZYLRGKFYVLGGRDENG
ONLTGGESYDEKTTWFELIPDILKDNSFSSYGSPPLIAVVGDDLYSLETSANEIRRYD
ANANSWKKLGDVPVRAKSNGGWGVAFKSLGDKLIAIGASAGPSRAETMSVYTSRPSAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :r because we remove overlaps between neighboring submissions.
clone is MOJ10 and the 3' clone is K17E12.
Location/Qualifiers
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for the latest information on annotation of this clone, please see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental
/product="serine/threonine phosphatase type 2c-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(2737. .4005)
/note="contains similarity to unknown protein emb|CAB55405.1
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/note="gene_id:MYF5.3
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18616. .19765,19862. .19966)
/note="gene_id:MYF5.4"
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/protein_id="BAB01932.1"
/db_xref="G1:9294080"
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/protein_id="BAB01933.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="Columbia"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /chromosome="3"
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/evidence=not\_experimental

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/note="predicted using Genefinder"
  Caenorhabditis elegans
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                                                                                                                                                                                                                                                        Direct Submission
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  ORGANISM
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                                                                                     AUTHORS
TITLE
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JOURNAL
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REMARK
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ALLWRTFFSTAVVVVVLREFIEICNSGKCGLFGKGGLIMFDVSHVTYTYHVTDIIPVM
LIGYTGGILGSELNHLLHKVLRLYNLINEKGK HKVLLSLITVSELFTSVCLGEPFELAK
CKPCDPSIDEICPTNGRSGENEKGFHCFKGYYNDLATLLITVDDAVRNLFSSNTPNEF
GMGSLWIFFVLIKCIIGLFFFGLATPSGLFLPTILMGAAYGRMLGAAMGSYTSIDQGLY
AVLGAAALMAGSMRMTVSLCVIFLELTNNLLLLPTTMIVLLIAKTVGDSFNPSITYDII
                                                                                                                                                                                                                                                                                                                           EREDNFDDVAITSAEMEMYVDLHPLTNTTPYTVMENMSVAKALVLFRQVGLRHLLIVP
CADASGMCPVVGILTRQDLRAYNILQAFPLLEKSKGGKTH"
COMPLEMENT(join(20497. 20704,20817. 20950,21039. 21380,
21519. 21632,21759. 221842,21918. 21997,22092. 22146,
22231. 22298,22378. 22422,22498. 22627,22716. 222830,
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                                                                                  LVGAKVSHIESELDYEINENDLEKHDWRKRSKAQVLQYVFLKWTLACLVGLFTGLIATL
INLAVENIAGYKLLAVGHFLTQERYVTGLMVLVGANLGLTLVASVLCVCFAPTAAGPG
IPEIKAYLNGVDTPNMFGATTMIVKIVGSIGAVAAGLDLGKEGPLVHIGSCIASLLGQ
                                                                                                                                                                                                                                                                                 LHIKGLPFLEANPEBWMRNLTVGELGDAKPPVVTLQGVEKVSNIVDVLKNTTHNAFPV
LDEAEVPQVGLATGATELHGLILRAHLVKVLKKRWFLTEKRRTEBWEVREKFPWDELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HADASVNPLSWIIGSDVVVVDPPRRGLDASLRQMLESVPSIEKRMRSSSQSSSLNAKE
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                                                                   translation="MVEEDLNQIGGNSNYNGEGGDPESNTLNQPLVKANRTLSSTPLA"
/product="CLC-d chloride channel; anion channel protein"
/protein_id="BAB01934.1"
/db_xref="GI:9294082"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.7%; Score 32.8; DB 8; Length 29176; 52.1%; Pred. No. 17;
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/protein_id="BAB01935.1"
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5015 c 4729 g 9715
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/note="emb|EAB12631.1
gene_id:MYF5.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 52.1
Matches 73; Conservative
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KEYWORDS
SOURCE
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current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.

Exceptions are indicated by an explicit note.

IMPORTANT: This sequence is not the entire insert of clone C49FB. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone C49FB is at 1 in this sequence. The true left end of clone F02Cl2 is at 39332 in this sequence. The true left end of clone F46Gl0 is at 1490 in this sequence. The start of this sequence (1. .1490) overlaps with the end of sequence 250177. The end of this sequence (39332. .39435) overlaps with the start of sequence 251269.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AQLSQYPQQANIIAQSTNPAQLDGLIALNNDAILALIGSFQSYSPSLLDSAPGTPPSG
FYPCAFSPVDQQMAVKI."
complement (join(12393. 12614,12767. 12955,13353. 13460,
13504. 13556,14826. 14886,15183. 15266,15849. 16375))
/gene="C49F8.1"
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dddrrahhnelerrrrdhikdhffilkdaipllldgekssralilkravefihvmqfkl
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13504. 13556,14826. 14866,15183. 15266,15849. 16375))
/gene="C49F8.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSQGKAIEDLTRKNELLEERLLERESSGSPSSSRLPALAVSSSQMQLTMPIIPQMQNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16-MAR-1996) Nematode Sequencing Project, Sanger Institute, Hinxton, Cambridge CB10 1SA, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu
Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other available information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       For a graphical representation of this sequence and its analysis see: http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(1006. .1201,1257. .1401,1454. .1727, 1779. .1871))
/gene="F46G10.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(1006. .1201,1257. .1401,1454. .1727,
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                                                                                                                                                                      Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                             The C.elegans Sequencing Consortium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="CAA94125.1"
/db_xref="GI:3875036"
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/chromosome="X"
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/gene="F46G10.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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21277 TCACCTATCTTGCTGTCGTCGTTTCAAAAGCATAAGGTCGTAGAACATATTATTTGGTCA 21218

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complement(join(37306. .37596,38318. .38467,38535. .38624))
/gene="C49F8.3"
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                                                                                                                                                                                                                                                 VSYLAFVAAFPTSNQQQYTQTAQQYPAQQEIKPSQTVPOLSAHHGYVYGPQQAMPQLS
QYPSPSTAAPAPVPEQPTLNNLPLEVKQSAQTLFNDPDFQMLARSLQSGTGSSGYSNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CaA94126.1"
/db_xref="G1:3875037"
/db_xref="SPTREMBL:017"
/translation="MSAKSNVQKFKIVFSFIHPDKIYLLVERLETPSESEMTARRRPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MRTRKKAEDVSCWVEHNQOPFSPSDEPRVRFEAPAPVSARSDDSDAESVESLTERPVY
KDGGYGWLVVLASFLMHAVCDGASFCFGIVFVKIQEHFQCGRFVSMITASMFLSLPLI
MSPVAGIVSDILGCRMSIIIGASICTVSCIIAMFCSHIFFFMISFGLGCGVGMSFIYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAIVIVTYYFEKRRGIATSFAVSGTGVGTVIYPILLNLSMIYLASFVSDIRIILIFFA
WYRVIAVI GFFIKNYFWESPKTDRFKLRRGOKTARNDDFFDRAISL
PNINILNHSGSIOSI TOSTERKSDRFKRRKSKVALFDNKHQMSSIPEYSMITNLA
NLEHLDLELANSPCTTVRAQRRRVISKVSMSVDQINELEDEAFHINLFQSSTESESDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MMRLTSCLLLAAFATYGFAQENGIDFDNPGNCGTEASNWKPCIE
RKVADQVFGSCCSRFVPPECRSLCIYETNAIEARVVLMHAIQPSRCRLYKYLPAIVHC
AAQTHDNSECCRSNGVAELGEQCVQMCQPQSNPRRFWGVKSLRKDMVVCLARWDQIMQ
                                                                                                                                                                            FSPSPLFSFGNCPYIFILLFHASSVREHHIMNSSQRRSIMFGEKAVIEMDIDPFVSNL
DTPADLKVPPTYTGPMLSTQLATPTMKKRDQNQNTHRDDEKKENNATEAGEPSAKKRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VAAGTSNMFGGRVIASNAIQSRHATNLIAMGKIPSAPMLVARKNRKSMIGKPIQGFYK
KWLETEKPIYQEVIHCRAYIYLALSVLCLYFILDVPYVCFYEYSIDTLKMEESBANYI
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/translation="MLNTKQNILNQRHCSQLKSLFTTAPFFQFTSDSLIFTNFPAKLI
                                                                                                                                              /SIFRSVCVQHMNFSFLSFSSSFFHFFSLHSFFTPPPFLPFLRLHFAYIHPYFFSRNN
                                                                                                                                                                                                                                                                                                                       LSARDIPPCSSDGRSVTIDHLRISPESLVQIARLAQAFGINPDWKKLRLADMKSALGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESSSDDSEMSNDGDSSSSELSEKNLDEPTTKLINKNLENVAFRATSSVPNSARMNRNS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .24671,
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                                                                                                                                                                                                                                                                                                                                                                                            .24671,
                                                                                                                                                                                                                                                                                                                                                                   complement(join(23105..23177,24031..24187,24238..24671
24759..25318.25734..26165,26214..26347,27098..27317,
27370..27597,27777..27881,28376..28456))
/gene="C49F8.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(23105. .23177,24031. .24187,24238. .2467
24759. .25318.25734. .26165,26514. .26347,27098. .27317,
27370. .27597,27777. .27881,28376. .28456))
/gene="c49F8.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Similarity to Hamster moncarboxylate transporter (SW:WOT1_CRILO), contains similarity to Pfam domain: PF01587 (Moncarboxylate transporter), Score=722.1, E-value=8.1e-214, N=1 CDN EST yk1494.3 comes from this gene CDNA EST yk294c8.3 comes from this gene CDNA EST yk294c8.5 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST yk294c8.5 comes from this gene
EST yk219b11.5 comes from this gene"
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/db_xref="GI:3875034"
/db_xref="SPTREMBL:Q18709"
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/protein_id="CAA94124.1"
/db_xref="GI:3875035"
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Direct Submission
Submitted (22-MAY-2000) Departments of Genomic Sciences and
Bioinformatics, Genetics Directorate, Glaxo Wellcome, Inc., 5 Moore
Drive, Research Triangle Park, North Carolina 27709-3398, USA
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                                                                                                                                                                                                                                      AF269928 3002 bp DNA linear BCT 01-AUG-2000 Staphylococcus epidermidis strain SR1 clone step.1032f01 genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 3002)
Kimmerly, W.J., Taylor, J. David., Nelsen, A.J., Godlevski, M.M.,
Rubino, M.A., Nelson, F.J., Rivers, P.R., Torruella-Miller, I..,
Listenbee, S., Asharti, C., Altshuller, G., Mamo, L., Shepherd, N.S.,
Fuchs, R., Fleming, T., Guan, X., Du, L., Cain, D. H., Miller, G.S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 3002)
Taylor,J.David., Kimmerly,W.J., Nelsen,A.J., Godlevski,M.M.,
Rubino,M.A., Nelson,F.J., Rivers,P.R., Torruella-Miller,I.,
Listenbee,S., Ashanti,C., Altshuller,G., Mamo,L., Shepherd,N.S.,
Fuchs,R., Fleming,T., Guan,X., Du,L., Cain,D.H., Miller,G.S. and
                           21217 ACTIGITITITITITAATIGGAATATCAAATIGCITIGITACAACAAAAATICGAAAAATIC 21158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transposon-mediated sequencing of the Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                627 ATTTAAGTGATTATCTTAGTATAGAAAATGCCTGAGACAATGATTGTCCCAGGCATTTTA 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             687 TTTATTGGCAATTGACAACGGAGTTGAACTTGGGCTAATCTCAATTTTCAACTCTAGTCC 746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
154 atttgtttttgcgcgatcggacggctgagttgatctggcgccaaaaacctctgctaagtc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus epidermidis
Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
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595 c 418 g 1
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51.4%;

Best\_Local Similarity 51.4 Matches 76; Conservative

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Query Match

Length 39435;

11.7%; Score 32.8; DB 3;

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Staphylococcus epidermidis strain SR1 clone step.1014906 genomic
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Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Staphylococcus.
1 (Dases I to 329)
Kimmerly, W. J., Taylor, J. David., Nelsen, A. J., Godlevski, M. M., Rubino, M. A., Nelson, F. J., Rivers, P. R., Torruella Miller, I., Listenbee, S., Asharti, C., Altshuller, G., Mamo, L., Shepherd, N. S., Fuchs, R., Fleming, T., Guan, X., Du, L., Cain, D. H., Miller, G.S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished
2 (bases 1 to 3295)
Taylor,JDavid., Kinmerly,W.J., Nelsen,A.J., Godlevski,M.M.,
Taylor,JDavid., Kinmerly,W.J., Nelsen,E.J., Torruella-Miller,I.,
Listenbee,S., Ashanti,C., Altshuller,G., Mamo,L., Shepherd,N.S.,
Fuchs,R., Fleming,T., Guan,X., Du,L., Cain,D.H., Miller,G.S. and
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11.5%; Score 32.4; DB 6; Length 3002;
Best Local Similarity 53.1%; Pred. No. 20;
Matches 69; Conservative 0; Mismatches 61; Indels 0
                                                                                                                                                 Staphylococcus epidermidis nucleic acids and proteins Patent: WO 0134809-A 3968 17-MAY-2001; GLAXO GROUP LIMITED (GB)
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/note="synthetic nucleic acid sequence"
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1 (bases 1 to 3002)
Kimmerly, W.J.
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Location/Qualifiers
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    3295 // Organism="synthetic construct" /db_xref="taxon:32630"

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Pred. No. 20;
0; Mismatches
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/clone="step.1014906"
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                                      1 (bases I to 3518)
Kimmerly, W.J., Taylor, J.David., Nelsen, A.J., Godlevski, M.M., Rubino, M.A., Nelson, F.J., Rivers, P.R., Torruella-Miller, I.., Listenbee, S., Asharti, C., Altshuller, G., Mamo, L., Shepherd, N.S., Fuchs, R., Fleming, T., Guan, X., Du, L., Cain, D. H., Miller, G.S. and
                                                                                                                                                                                                                               Taylor, J. David., Kimmerly, W.J., Nelsen, A.J., Godlevski, M.M., Rubino, M.A., Nelson, F.J., Rivers, P.R., Torruellar Miller, I.., Listenbee, S., Ashanti, C., Altshuller, G., Mamo, L., Shepherd, N.S., Fuchs, R., Fleming, T., Guan, X., Du, L., Cain, D.H., Miller, G.S. and
                                                                                                                                                     Transposon-mediated sequencing of the Staphylococcus epidermidis
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    Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Staphylococcus.
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/db_xref="taxon:32630"
/note="synthetic nucleic acid sequence"
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                                                                AUTHORS
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11.5%; Score 32.4; DB 6; Length 3518;

Query Match

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Direct Submission
Submitted (22-MAY 2000) Departments of Genomic Sciences and
Bioinformatics, Genetics Directorate, Glaxo Wellcome, Inc., 5 Moore
Drive, Research Triangle Park, North Carolina 27709-3398, USA
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Taylor, J.David., Kimmerly, W.J., Nelsen, A.J., Godlevski, M.M.,
Rubino, M.A., Nelson, F.J., Rivers, P.R., Torruella-Miller, I.,
Listenbee, S., Ashanti, C., Altshuller, G., Mamo, L., Shepherd, N.S.,
Fuchs, R., Fleming, T., Guan, X., Du, L., Cain, D.H., Miller, G.S. and
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Kimmerly, W.J., Taylor, J. David., Nelsen, A.J., Godlevski, M.M., Rubino, M.A., Nelsen, F.J., Rivers, P.R., Torruella-Miller, I., Listenbee, S., Ashanti, C., Altshuller, G., Mamo, L., Shepherd, N.S., Fuchs, R., Fleming, T., Guan, X., Du, L., Cain, D.H., Miller, G.S. and
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11.5%; Score 32.4; DB 6; Length 3985;
Best Local Similarity 53.1%; Pred. No. 20;
Matches 69; Conservative 0; Mismatches 61; Indels 0;
                                                                                               synthetic construct.
synthetic construct
artificial sequence.
1 (bases 1 to 3985)
Kimmerly,W.J.
Staphylococcus epidermidis nucleic acids and proteins
Patent: WO 0134809-A 3856 17-MAY-2001;
GLAXO GROUP LIMITED (GB)
LOCALION/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="synthetic nucleic acid sequence"
779 c 583 g 1448 t
                              AX145134 3985 bp Db Sequence 3856 from Patent W00134809. AX145134 AX145134.1 GI:14283699
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Gemini virus DNA f
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                                                                                                                                                                                                        1 aatcgagttatgggggggcc........ccccaacctctgctaacccc 281
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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## ALIGNMENTS

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AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (II) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the soft action of vectors on taining them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) via the production of vectors polypeptides and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55091 represent specifically claimed S. epidermidis genomic DNA AAH55091 to Polymucleotide sequences from the present invention. AAH55091 to AAH55098 represent oligonucleotide sequences and primers which are used in man and primers which are used to the exemplification of the present invention.
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N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
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53.1%; Pred. No. 0.54;
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Claim 8; Page 1634-1635; 2188pp; English.
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AMES 304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis.

(I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the pulypeptides may also be used to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH33971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polymoclectide sequences and primers which are used in the exemplification of the present invention. AAH55091 to AAH55099 represent oilygonuclectide sequences and primers which are used in the exemplification of the present invention.

CN.B. The present invention specifically claims all the polymoclectide exequences is given in the sequence listing of the present specification. Chowever the sequence listing only goes up to SEQ ID NO:4454 so even consequences.
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useful for vaccinating against infections, e.g. endocarditis
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                                                                                                                       Claim 8; Page 1285-1287; 2188pp; English.
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AAH55304 to AAH53970 represent nucleic acids (I) encoding polypeptides CC (II), given in AAG81454 to AAG81120, from Staphylococcus epidermidis. CC (II) and (II) can have antibacterial activity and therefore can be used to recination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the coordinate subjects and to raise antibodies against then be polypeptides may also be used to assay for other inhibitors of their The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the activity and therefore identify compounds that may be used for the AAB5509 represent specifically claimed S. epidermidis genomic DNA AAB5509 represent specifically claimed S. epidermidis genomic DNA AAB5509 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention. AAB5509 to sequence listing of the present specifically claims all the polynucleotide sequence listing of the present specification, chowever the sequence listing of the present specification, however the sequence listing of the present specification, however the sequence listing of the present specification, chowever the sequence listing of the present specification, however the sequences are given in the disclosure for SEQ ID NO:4454 so even though sequences are present for SEQ ID NO:4455 to 4472, on sequences are present for SEQ ID NO:4455 to 4472,
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    Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 53.1%; Pred. No. 0.58;
Matches 69; Conservative 0; Mismatches 61; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S. epidermidis genomic polynucleotide sequence SEQ ID NO:3856.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination; endocarditis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3518 BP; 1091 A; 677 C; 495 G; 1255 T; 0 other;
                                                                         Claim 8; Page 1808-1809; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH54492 standard; DNA; 3985 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-NOV-2000; 2000WO-US30782.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2710 tcattaccaa 2719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220 taagtataaa 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200134809-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kimmerly WJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-MAY-2001.
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AAH55204 to AAH53970 represent nucleic acids (I) encoding polypeptides CC (II), given in AAG81454 to AAG81120, from Staphylococcus epidermidis. CI ) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the coordance onlypeptides (II) via the production of vectors to solypeptides (II) (and/or nucleic acids) may then be colypeptides may also be used to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their crap polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the cramment of S. epidermidis infections, e.g. endocarditis. AAH55091 to polynucleotide sequences from the present invention. AAH55091 to polynucleotide sequences and primers which are used the present invention of the present invention. AAH55091 to sequence listing of the present specification, sequence listing of the present specification, sequence listing of the present specification. And sequence listing of the present specification, sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4465 to 4472, consequences are present for SEQ ID NO:4465 to 4472, consequences are present for SEQ ID NO:4465 to 4472, consequences are present for SEQ ID NO:4465 to 4472, consequences are present for SEQ ID NO:4465 to 4472, consequences are present for SEQ ID NO:4465 to 4472, consequences are present for SEQ ID NO:4465 to 4472, consequences are present for SEQ ID NO:4465 to 4472, consequences are present for SEQ ID NO:4465 to 4472, consequences are present for SEQ ID NO:4465 to 4472, consequences are present for SEQ ID NO:4465 to 4472, consequences are present for SEQ ID NO:4465 to 4472, consequences are present for SEQ ID NO:4465 to 4472, consequences are present specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           381 atttaagtgattatettagtatagaaaatgeetgagaeaatgattgteeeaggeatttta 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 ttttgcgcgatcggacggctgagttgatctggcgccaaaaacctctgctaagtcccgtgc 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis; strain H37Rv; strain CDC 1551; genome; variation; epidemiology; patient treatment; epidemic monitoring; ds.
                                                Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.5%; Score 32.4; DB 22; Length 3985; 53.1%; Pred. No. 0.61; Live 0; Mismatches 61; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis strain H37Rv genome SEQ ID NO 1.
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                                                                                                                                 Claim 8; Page 1500-1502; 2188pp; English.
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hes 69; Conservative
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             WPI; 2001-316495/33.
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The invention relates to evaluating strain variation within and between different populations of the tuberculosis bacterial pathogen, wycobacterium tuberculosis or related Mycobacterium by determining the nucleotide sequence of the first strain at positions in the complete sequence of the genome that correspond to positions that differ in the nucleotide sequences of M. tuberculosis strains CDC 1551 (AA199683) and H37Rv (AA199682). The method is useful for evaluating strain variation of tuberculosis and has valuable application in the fields of tuberculosis genetics, epidemiology, patient treatment and epidemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, cytokine, cell proliferation, cell differentiation; gene therapy; vaccine, peptide therapy, stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4411529 BP; 758565 A; 1449983 C; 1444602 G; 758379 T; 0 other;
                                                                                       Evaluating strain variation of Mycobacterium tuberculosis, comprises determining the nucleotide sequence of the strain at positions in the genome corresponding to positions where M. tuberculosis strains CDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 gagtagettgetggagaagaagcegcaagcetetatetacegtecatttgtttttgege 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.5%; Score 32.2; DB 22; Length 4411529; 57.4%; Pred. No. 15; tive 0; Mismatches 43; Indels 0; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 3577668 GCACTGTTTGCCGGGCGGCAGCGAGTCCCAACTGCT 3577628
                                                                                                                                                                              Claim 3; SEQ ID NO 1; 3pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                  at seqdata.uspto.gov/sequence.html?DocID=6294328B1.
                   Fleischmann RD, White OR, Fraser CM, Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  168 gatcggacggctgagttgatctggcgccaaaaacctctgct 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human polynucleotide SEQ ID NO 6885.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAI86825 standard; cDNA; 460 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tang YT, Liu C, Drmanac RT;
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18-MAY-2000; 2000US-0577409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58; Conservative
                                                                                                                                                1551 and H37Rv differ
                                                     WPI; 2001-647261/74.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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The invention relates to human polynucleotides (AA179941-AA193841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine. cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or e.g. stem cell growth factor activity, hematopoiesis regulating activity itssue growth factor activity, immunomodulatory activity and activity and may be useful in the diagnosis and/or
                                                                                                                                                                                                                                                                                                                       Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                       treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85 ctttccacgtcaccaatccaggtgagtagcttgctggagaagaagacgcaagcctctat 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               377 CITGATACATIGCCAAGCCIGGICTCAAGCITIGGCAICAAGCAAICCIGGCCCICAGC 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145 ctaccgtccatttgttttgcgcgatcggacggctgagttgatctggcgccaaaaacctc 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                317 CICCCAICAIGCIGGGAITACAGGIGCACTCAGCCIATAAGGGGGITTIGCCITCCAGITC 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205 tgctaagtcccgtgctaagtataaatagccgcgggggctagtattacccccgcgggtccc 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coconut Foliar Decay Virus; CFDV; strong promoter; tissue-specific; phloem-specific; stem-loop structure; transgenic plant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "loop has homology to geminivirus sequence"
                                               diagnosing and treating e.g. leukaemia, inflammation and immune
                                Isolated nucleic acids and polypeptides, useful for preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                           11.2%; Score 31.4; DB 22; Length 460; 48.1%; Pred. No. 0.55; tive 0; Mismatches 96; Indels 0
                                                                                              Claim 1; SEQ ID NO 6885; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 460 BP; 114 A; 115 C; 141 G; 88 T; 2 other;
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 P-PSDB; AAO06894.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 TGCCC 193
                                                                                                                                                                                                                                                                                                         inflammation
                                                                   disorders -
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                                                                                  activity in E. coli than the CaMV 35S promoter
                                                                                                  Sequence 31 BP; 5 A; 11 C; 11 G; 4 T; 0 other;
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                                                                                                                                                                 231 agccgcggggggctagtattacccccgcggct 261
                                                                                                                                                                           Gemini virus DNA fragment stem loop.
                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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Disclosure; Fig 2; 14pp; German.
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                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                 31; Conservative
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                                                                                                                                          Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                        Gemini virus.
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                                                                                                                                                                                                                                                                         10-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                   stem_loop
                                                                                                                                                                                                                                                     AAX02686;
                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                      Stem loop; coconut foliar decay virus; CFDV; bacterial promoter; ss. yeast promoter; tissue-specific; phloem-specific; CaMV 35S promoter; ss.
                                                                                                                                 A DNA fragment from the CFDV genome can be used as a phloem-specific promoter in the construction of transgenic plants. The promoter is strong; it has 30-50% of the activity of the CaMV 35S promoter in
                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Coconut foliar decay virus promoters - for gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to 31"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21..31 /*tag= c /note= "Region binds to nucleotides 1 to 11"
                                                                                                                                                                                                        11.0%; Score 31; DB 15; Length 31; 100.0%; Pred. No. 0.23; Live 0; Mismatches 0; Indels
                                                                                     Use of coconut foliar decay virus DNA as promoter - for tissue-specific gene expression in transgenic plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Region binds to nucleotides 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Salamini F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
                                (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN
                                                                                                                                                                                 Sequence 31 BP; 5 A; 11 C; 11 G; 4 T; 0 other;
                                                 Salamini F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rohde W,
                                                                                                                                                                                                                                                Gemini virus DNA fragment stem loop.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                  Rohde W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Randles JW,
                                                                                                                                                                                                                                                                                                                 AAX02688 standard; DNA; 31 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97DE-1030502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97DE-1030502
                                                                                                                  Claim 1; Fig 2; 8pp; German.
              93DE-4306832
                                                                                                                                                                                                                                                                                                                                                     10-MAY-1999 (first entry)
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                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1..11
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
                                                    Randles JW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-096863/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bacteria and yeasts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hehn A,
                                                                    WPI; 1994-058406/08
                                                                                                                                                                 tobacco plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DE19730502-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                     Gemini virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_binding
               04-MAR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JAN-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Becker D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                stem_loop
                                                    Becker D,
                                                                                                                                                                                                                                                                                                                                     AAX02688;
                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                         AAX02688/c
                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                   δλ
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This invention describes a coconut foliar decay virus (CFDV) DNA fragment that includes the stem-loop structure of CFDV DNA but lacks the translation start codons of open reading frames ORF1 and/Or ORF2. The new CFDV DNA fragment is useful as a bacterial or yeast promoter, as a promoter for tissue-specific (especially phloem-specific) gene expression in plants and for production of chimeric constructs for translent or
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This invention describes a coconut foliar decay virus (CFDV) DNA fragment that includes the stem-loop structure of CFDV DNA but lacks the translation start codons of open reading frames ORF1 and/or ORF2. The new CFDV DNA fragment is useful as a bacterial or yeast promoter, as a promoter for tissue-specific (especially phoem-specific) gene expression in plants and for production of chimeric constructs for transient or stable expression. Certain fragments of CFDV DNA have stronger promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stem loop; coconut foliar decay virus; CFDV; bacterial promoter; ss. yeast promoter; tissue-specific; phloem-specific; CaMV 35S promoter; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     b
"Region binds to nucleotides 21 to 31"
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"Region binds to nucleotides 1 to 11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.0%; Score 31; DB 20; Length 31; 100.0%; Pred. No. 0.23; tive 0; Mismatches 0; Indels
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and parasitic infections.

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49 human secreted proteins AAB32050. The genes can be used to generate fusion proteins by linking to the gene for the human content fusion proteins by linking to the gene for the human common debuling Fr portion (SEQIDI) for increasing the stability of the fusion protein as compared to the human protein only. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and concer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune colliss, remunential and ulcerative colliss; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fundal
                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antibarasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; ss.
  stable expression. Certain fragments of CFDV DNA have stronger promoter activity in E. coli than the CaMV 355 promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to the isolation of genes AAC66410-C66458 encoding
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid molecules encoding human secreted proteins, used in
                                                                                                                                                                    ö
                                                                                                                     11.0%; Score 31; DB 20; Length 31; 100.0%; Pred. No. 0.23; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human secreted protein coding sequence SEQ ID NO: 17.
                                                          Sequence 31 BP; 5 A; 11 C; 11 G; 4 T; 0 other;
                                                                                                                                                                                                   231 agccgcgggggctagtattaccccggggct 261
                                                                                                                                                                                                                        Komatsoulis G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 337; 423pp; English.
                                                                                                                                                                                                                                                                                                                                          AAC66416 standard; DNA; 974 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-MAR-2000; 2000WO-US07483.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0126596.
99US-0171552.
                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                        Best Local Similarity 100.(
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-602357/57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAB32008.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                        14-FEB-2001
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                                                                                                                                                                                                                                                                                                                                                                                  AAC66416;
                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                    RESULT 10
                                                                                                                                                                                                                                                                                                                         AAC66416/
SSXS
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The sequences given in AAQ47709-10 represent embryo and liver derived human transforming growth factor-beta (TGF-beta) genes repectively. The proteins encoded by these sequences may be used in a pharmaceutical composition for the treatment of various bone, cartilage or tooth defects and in tissue and wound repair processes. These proteins may also be used as immunosuperssors in organ transplants and in cosmetic surgery. Antibodies raised against these proteins may be
                                                                                                                                          138 cctctatctaccgtccatttgtttttgcgcgatcggacggctgagttgatctggcgccaa 197
                                                                                                                                                                          441 CCTCTAAGATCCCTTCAACTCCGAATCTCTGATTTGACTGCAGGAAAACAAGCCCTAG 382
                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; transforming growth factor; beta; TGF-beta; pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New transforming growth factor-beta family proteins and DNA -used in tissue and wound repair, in treatment of bone, cartilage and tooth defects, and antibodies for diagnosis
                                                                                                              ö
                                                                                Length 974;
                                                                                                                                                                                                          198 aaacctctgctaagtcccgtgctaagtataaatagccgcgggggctagtatt 249
                                                                                                                                                                                                                                         381 AAACAIGGGTTACAGCCIGGGCTAGGCTTGCTTAGCGGCCAGGGCAGGTTTT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cartilage; tooth; wound repair; immunosuppressor; transplant; cosmetic surgery; antibody; diagnosis; ss.
                                                                                                              Indels
                            Sequence 974 BP; 229 A; 252 C; 263 G; 230 T; 0 other;
                                                                                                             51;
                                                                            Score 30.4; DB 21;
Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 265 BP; 58 A; 80 C; 69 G; 58 T; 0 other;
                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                      AAQ47710 standard; cDNA to mRNA; 265 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 18; 29pp; English.
                                                                            10.8%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cosmetic surgery. Antibodies used for diagnostic purposes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92EP-0102324.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93WO-EP00350.
                                                                                                                                                                                                                                                                                                                                                                                                                       TGF-beta-like clone MP-121.
                                                                                                                                                                                                                                                                                                                                                                                     11-FEB-1994 (first entry)
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                                                                                                             61; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag=
                                                                                             Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-FEB-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hoetten G,
                                                                                                                                                                                                                                                                                                                                                        AAQ47710;
                                                                              Query Match
                                                                                                                                                                                                                                                                                         RESULT 11
                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                                        AAQ47710
SXC
                                                                                                                                                                          q
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Score 30; DB 14; Length 265; Pred. No. 1.4;

10.7%; 59.3%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a degenerate sequence which encodes a human disintegrin homologue, designated zdintl. The zdintl polypeptide is a cardiac myocyte proliferation and differentiation stimulator, as well as an adipocyte proliferation and differentiation inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptide is also useful in identifying its new family members, antagonists, agonists and antibodies. Antagonists, antibodies and fusion proteins of zdintl are useful in inhibiting platelet aggregation, apoptosis, neurogenesis and myogenesis. Agonists and antagonists are
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; disintegrin homologue; zdintl; cardiac myocyte; adipocyte; gene therapy; cell-cell interaction; chondro sacroma; atherosclerosis; Alzheimer's disease; restenosis; ischemic repertusion; obesity; intimal hyperplasia; tumour; platelet aggregation; apoptosis; neurogenesis; myogenesis; arthritis; myogenesis; neurogenesis; connective tissue disorder; chondrogenesis; tumour proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful in studying cell-cell interactions, arthritis, myogenesis, neurogenesis, connective tissue disorders, chondrogenesis, tumour proliferation and suppression, extracellular matrix proteins, repair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and remodelling of ischemic reperfusion, inflammation, and apoptosis.
                                          192 egecaaaaaectetgetaagteeegtgetaagtataaatageegegggggtagtattae 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polypeptide useful in modulating cell-cell interaction in tissues of heart, brain, spinal cord and treating chondro sarcoma, atherosclerosis, restenosis, obesity, intimal hyperplasia and tumors
Gaps
                                                                                 19 egecatgaaettetgeatagggeagtgeeceactaeacatageaggeatgeetggtattge 78
                                                                                                                                                                                                                                                                                                                                                                                                   Degenerate DNA encoding a disintegrin homologue designated zdintl
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  35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Deisher TA, Bishop PD;
  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 129-130; 132pp; English.
                                                                                                                            ccccgcggctccccaacctctgctaa 277
                                                                                                                                                                   79 tgcctcctttcacactgcagtgctca 104
                                                                                                                                                                                                                                                                            BP
                                                                                                                                                                                                                                                                         AAZ45827 standard; DNA; 2088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US15638.
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                                                                                                                                                                                                                                                                                                                                                             (first entry)
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  51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-160898/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inflammation; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                      AAZ45827;
    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; disintegrin; zdintl; ds; antiangiogenic; vascular; thrombolytic. cell matrix; cell-cell interactions; apoptosis; neurogenesis; connective tissue disorders; chondrogenesis; arthritis; tumour proliferation; ischaemia reperfusion; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated novel disintegrin protease family
                                                                      gettgeagtgeaegeaaceaettteeaegteaeceaateeaggtgagtagettgetggaga 124
                                                                                                                                             125 agaaagccgcaagcctctatctaccgtccatttgtttttgcgcgatcggacggctgagtt 184
                                                                                                           190 GYTTNCCRTTYTCRTARTGDATYTCNACRTARTCNSWNSWNARNARNCCRTTRTTNARDA 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disintegrins protease zdintl, useful for producing agents for the development of antithrombotic and anti-migration of tumour cells and
                                        Gaps
                                                                                                                                                                                 130 TNARRICNARDATRAAYTINSWNCCRAANGCYTCDATYIGRAANSWNGCYIGNGCNARRI 71
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0
   Length 2088;
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                                        Indels
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                                                                                                                                                                                                                        185 gatctggcgccaaaacctctgctaagtcccgtgctaagtataaa 229
                                                                                                                                                                                                                                           Human degenerate DNA for disintegrin protease zdintl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Deisher TA, Bishop PD,
   DB 21;
10.7%; Score 30; DB 27.9%; Pred. No. 3.4; Live 36; Mismatches
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                                                                                                                                                                                                                                                                                                                                                    AAS11992 standard; DNA; 2088 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            have antiangiogenic activity
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                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
   Query Match
Best Local Similarity 27.99
Matches 46; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromosome 2q33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                 gettgeagtgeacgeaaccactttceacgteaccaatceaggtgagtagettgetggaga 124
                                                                                                                                                                   125 agaaagccgcaagcctctatctaccgtccatttgtttttgcgcgatcggacggctgagtt 184
                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGF-beta; MP-121; mitogen; differentiation; induction; promotion; maintenance; morphogen; tissue regeneration; dental implantation;
                                                                          ;
      DB 22; Length 2088;
                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                185 gatctggcgccaaaaacctctgctaagtcccgtgctaagtataaa 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2272 BP; 510 A; 663 C; 513 G; 586 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 GNACNGCYTTRTTRTGYTTYTGYTGRTGNCKNGCYTTNGTRTCNA 26
                                                                    83;
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                                                                36; Mismatches
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/product= TGF-beta_MP-121
836..1183
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10.7%; Score 30; 27.9%; Pred. No.
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                                                                    Conservative
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nes 46; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "transforming growth factor (TGF)-beta monomeric
                                                                                                                                           192 cgccaaaaacctctgctaagtcccgtgctaagtataaatagccgcggggggctagtattac 251
                                                                                                                                                                                Novel monomeric protein of transforming growth factor-beta family for prevention or therapy of diseases associated with bone, cartilage damage, promotion of wound healing, has substitution or deletion of eysteine
                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; transforming growth factor-beta; monomeric protein; MP52; MP121; dimeric protein; TGF-beta; vulnerary; antiulcer; nootropic; neuroprotective; antiinfertility; osteopathic; gene therapy; bone; cartilage; dental; wound healing; connective tissue; ds.
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Score 30; DB 17; Length 2272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human TGF-beta MP121 nucleotide sequence SEQ ID NO:3.
                                                                         35;
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                                    Pred. No. 3.5;
                                                                  0; Mismatches
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                                                                                                                                                                                                                                                                                    252 ccccgcggctccccaacctctgctaa 277
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/product= "MP121"
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59.3%;
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                                    Similarity
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Sequence 1, A
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Sequence 228,
Sequence 2, A
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-351-414-3

US-08-482-577B-1

US-08-482-577B-1

US-08-481-77B-1

US-09-218-176-1

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US-08-655-836-2

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Listing first 45 summaries
                                                            OM nucleic - nucleic search, using sw model
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Sequence 19, Appl Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 6, Appli Sequence 5, Appli Sequence 10, Appli Sequence 11, Appli Sequence 11, Appli Sequence 12, Appli Sequence 11, Appli	uence:/note=syntheti Length 1291; indels 0; Gap ataagaacgaatctgtta 6	agaagaaagccgcaagcctctatctaccgtccatttgttttgcgcgatcggacggctg 180
4 US-09-202-712-19 1 US-08-323-531-1 1 US-08-198-094-1 4 US-08-198-094-1 5 PCT-US93-07424-1 5 PCT-US93-07424-1 4 US-07-861-458C-6 4 US-07-861-458C-6 4 US-07-861-458C-6 4 US-09-307-678B-48 4 US-09-307-678B-48 5 PCT-US96-053-05-1 7 US-09-020-956-17-15 4 US-09-020-956-17-15 4 US-09-020-956-17-15 4 US-09-020-956-17-15 4 US-09-020-956-17-15 4 US-09-020-956-17-15	ALIGNMENTS  DNA AS A PRO  462,975  98/04345  02.4  rsion 4.0  red. No. 4.1e  mismatches  aaaagattccatt                   aaaagattccatt  ttccacgtcacca  ttccacgtcacca	ctatctaccgtccatttgt
.5 1447 .5 1322 .5 1322 .5 1322 .5 1322 .6 1322 .7 1013 .4 1131 .4 4212 .4 4212 .4 4212 .4 4212 .3 740 .3 740	SULT 1 Sequence 1, Application US/09462975 Sequence 1, Application US/09462975 Sequence 1, Application US/09462975 Sequence 1, Application US/09462975 GENERAL INFORMATION: APPLICANT: Rendles, John W. APPLICANT: Randles, John W. APPLICANT: Salamini, Francesco TITLE OF INVENTION: USE OF VIRUS I FILE REFERENCE: 2323.0003u1 CURRENT APPLICATION NUMBER: US/09/07-07-07-07-07-07-07-07-07-07-07-07-07-0	geegeaageet
00000000000000000000000000000000000000	ULT 1  equence 1, Applicatio atent No. 6303345: APPLICANT: Rohde, Wo APPLICANT: Rendles, APPLICANT: Becker, D APPLICANT: Bannin, TILLE OF INVENTION: CURRENT APPLICATION NUM PRIOR FILING DATE: 1 PRIOR FILING DATE: 1 PRIOR FILING DATE: 1 PRIOR FILING DATE: 1 NUMBER OF SEQ ID NOS: SOFTWARE: FastSEQ fo EQ ID NO 1 LENGTH: 1291 TYPE: DNA Artificial FEATURE: OTHER INFORMATION: C O9-462-975-1  uery Match est Local Similarity atches 191: Conserv	ъ –
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Sequence 8, A Sequence 7, A Sequence 8, A

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                                                                                                                                     APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence:/note=synthetic; OTHER INFORMATION: construct
US-09-462-975-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 57.4%; Pred. No. 1.5;
Matches 58; Conservative 0; Mismatches 43; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 3577668 GCACTGTTTGCCGAGCCGGCCAGGAGCGAATCCCAACTGCT 3577628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09462975

Fatent No. 6303345

GENERAL INFORMATION:
APPLICANT: Rohde, Wolfgang
APPLICANT: Radder, Dieter
APPLICANT: Becker, Dieter
APPLICANT: Becker, Dieter
APPLICANT: Hehn, Alain
APPLICANT: Salamin, Francesco
TITLE OF INVENTION: USE OF VIRUS DNA AS A PROMOTER
FILE REFERENCE: 23222.000311
CURRENT APPLICATION NUMBER: US/09/462,975
CURRENT APPLICATION NUMBER: PCT/EP98/04345
PRIOR APPLICATION NUMBER: 1998-07-13
PRIOR APPLICATION NUMBER: 1977-07-16

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 gatcggacggctgagttgatctggcgccaaaaacctctgct 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43;
                                                                                                                                                                                                                                                   TILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) ORGANISM: Mycobacterium tuberculosis
) OTHER INFORMATION: H37Rv
US-09-103-840A-1
                                          Sequence 1, Application US/09103840A Patent No. 6294328
                                                                                          GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match
Best Local Similarity 100..
Pest Local 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 4411529
                 US-09-103-840A-1/C
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LENGTH: 31
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
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192 cyccaaaaacctctyctaaytcccytyctaaytataaatayccgcggggggtagtattac 251
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                                                                                                                                                                          TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B TITLE OF INVENTION: FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                                                                                                                                                                                                                                                               ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
STREET: SUITE 330
                                                                                                                                                                                                                                                                                                                                                                                                                                SUFTWARE: DETENTING PC DOS/MS-DOS SUFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/289,222E FILING DATE: 25-AUG-1999 CLASSIFICATION: 424 PRIOR APPLICATION: -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: DE P 44 23 190.3 FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA: APPLICATION NUMBER: EPO 92102324.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/ED93//////FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/EP93/00350 FILING DATE: 12-FEB-1993 ATTORNAL ANNUMBER: MANNUMBER: PCT/EP93/00350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36,105
ER: P564-9021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                252 ccccgcggctccccaacctctgctaa 277
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                    ; Sequence 5, Application US/08289222E
; Patent No. 6120760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PSS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: cDNA from mRNA
                                                                                                       APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLE
APPLICANT: POHL, JENS
                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                         HOTTEN, GERTRUD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: KITTS, MONICA CHIN REGISTRATION NUMBER: 36,1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            265 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202/638-4810
                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 5:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
                                                                                                                                                                                                                                                                                                                               WASHINGTON
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                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              USA
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US-08-289-222E-5
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                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                    CITY:
STATE:
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231 agccgcgggggctagtattacccccgcggct 261

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US-09-351-414-3/c
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                                                                           Sequence 5, Application US/09054526B
Patent No. 6197550
GENERAL INFORMATION:
APPLICANT: H TTEN, GERTRUD
APPLICANT: BECHTOLD, ROLF
APPLICANT: DOLL, JENS
TITLE OF INVENTION: GROWTH/DIFFERENTATION FACTORS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIFAIDO, MARMELSTEIN, MURRAY & ORAM LLP
STREET: 555 FIFTEENTH STREET, N. W., G STREET LOBBY,
STREET: SUITE 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 265;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,526B
FILING DATE: U3/03/09/054,526B
FILING DATE: U3/03/09/054,526B
FILING DATE: U3/03/09/04
PRIOR APPLICATION NUMBER: U5/08/222
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 12-806 10-10L-1994
PRIOR APPLICATION NUMBER: EPO 92102324.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION NUMBER: POP 92102334.8
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: POT/FEP93/00350
APPLICATION NUMBER: POT/FEP93/00350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 30; DB 4;
Pred. No. 0.066;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: KITTORNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36,105
ER: P564-8005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA from mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 202/5/38-4810
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match
Local Similarity 59.3%;
hes 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 265 base pairs
nucleic acid
EDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                       WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                             RY: USA
20005-5701
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                                 RESULT 5
US-09-054-526B-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
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RESULT

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65 gettgeagtgeaegeaaceaettteeaegteaeceaateeaggtgagtagettgetggaga 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: zdint1 amino acid degenerate sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 gatctggcgccaaaaacctctgctaagtcccgtgctaagtataaa 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: NIKAIDO, MARMELSTEIN, MURRAY, AND ORAM STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY, STREET: SUITE 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 GNACNGCYTTRITRIGYTYTYTGYTGRIGNCKNGCYTTNGTRTCNA 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS CORRESPONDENCE. 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATINE SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 10.7%; Score 30; DB 4; Best Local Similarity 27.9%; Pred. No. 0.19; Matches 46; Conservative 36; Mismatches
                                         APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Baindur, Nand
APPLICANT: Baindur, Nand
APPLICANT: Bishop, Paul D.
TITLE COF INVENTION: DISINTEGRIN HOMOLOG
FILE REFERENCE: 38-29
CURRENT APPLICATION NUMBER: US/09/351,414
CURRENT FILING DATE: 1999-07-09
NUMBER OF SEO ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: variation
LOCATION: (1)...(2088)
OTHER INFORMATION: n is any nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08482577B Patent No. 5807713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (1)...(2088)
OTHER INFORMATION: n = A,T,C or G
Sequence 3, Application US/09351414
Patent No. 6265199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HOTTEN, GERTRUD
APPLICANT: NEIDHENOT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
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Gaps

us-09-462-955b-1\_copy\_711\_991.rni

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B
TITLE OF INVENTION: FAMILY
NUMBER OF SEQUENCES; 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
10.7%; Score 30; DB 1; Length 2272;
Best Local Similarity 59.3%; Pred. No. 0.2;
Matches 51; Conservative 0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: BOTH STREET, N. W., G STREET LOBBY, STREET: STREET STREET NO W., G STREET LOBBY, CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ELICATION NUMBER: US/08/289,222E
FILING DATE: 25-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
PRIOR APPLICATION NUMBER: DF 94 23 190.3
FILING DATE: 07-JUL-1994
PRIOR APPLICATION NUMBER: EPO 92102324.8
FILING DATE: 12-FEB-1992
                                                                                                                            36,335
ER: P564-5010
                    APPLICATION NUMBER: US/08/482,577B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1000 recercerreacacrecaerce 1025
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COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08289222E Patent No. 6120760
                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KLESNER; SHARON
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P564-
TELEPHONE: 202/638-5000
TELEPHONE: 202/638-5000
TELEFRA: 202/638-6100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2272 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: HOTTEN, GERTRUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-289-222E-2
                                                                                                                                                                                                                                                                                                                                                                                     US-08-482-577B-1
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192 cgccaaaaacctctgctaagtcccgtgctaagtataaatagccgcggggggtagtattac 251
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APPLICANT: BECHTOLD, Rolf
APPLICANT: POHL, Jens
APPLICANT: POHL, Jens
APPLICANT: POHL, Jens
TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE
TITLE OF INVENTION: TGF- FAMILY
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.7%; Score 30; DB 3; Length 2272; 59.3%; Pred. No. 0.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: NIKAIDO, MARWELSTEIN, MURRAY & ORAM LLP STREET: 655 Fifteenth Street, N. W., G Street Lobby STREET: Suite 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
CURLIANTION NUMBER: US/09/218,176
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                       REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-9021
TELEPOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEPAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGH: 2272 base pairs
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APPLICATION NUMBER: PCT/EP96/03065
FILING DATE: 12-JUL-1996
PRIOR APPLICATION DATA: PCT/EP93/00350
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 2-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350 FILING DATE: 12-FEB-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1000 IGCCICCITICACACIGCAGIGCICA 1025
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APPLICATION NUMBER: 08/679,048
FILING DATE: 12-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-218-176-1; Sequence 1, Application US/09218176; Patent No. 6171584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA from mRNA US-08-289-222E-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 10.7%;
Best Local Similarity 59.3%;
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: H TTEN, Gertrud
                                                                             NAME: KITTS, MONICA CHIN REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Washington
                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: HTTEN, GERTRUD
APPLICANT: HELGE
APPLICANT: BECHTPULD, ROLF
APPLICANT: POHL, JENS
TITLE OF INVENTION: GROWTH/PIFFERENTATION FACTORS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE SDIRESS:
ADDRESSE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
CITY: MASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                          APPLICATION NUMBER: EP 92 102 324.8
FILING DATE: 12-FEB 1992
PRIOR APPLICATION DATE: 1994
APPLICATION DATE: DE P 44 23 190.3
FILING DATE: 01-JUL-1994
PRIOR APPLICATION DATE: DE PILOR DATE: 20-JUL-1994
APPLICATION NUMBER: DE 195 11 243.1
FILING DATE: 27-MAR-1995
ATTORNEY, FAGENT INFORMATION:
NAME: KITTS, MODICAE CHIN
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-6010
TELECHONE: 202/638-5000
TELECHONE: 202/638-5000
TELECHONE: 202/638-8000
INFORMATION FOR SEQ 1D NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2272 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,526B
FILING DATE: 03-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1000 recercertreacacrecaerecre 1025
APPLICATION NUMBER: US 08/482,577 FILING DATE: 7-JUN-1995 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09054526B Patent No. 6197550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
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US-09-054-526B-2
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192 cgccaaaaacctctgctaagtcccgtgctaagtataaatagccgcggggggtagtattac 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 cgagttatgggcgggcccacaataaaagattccatttggataagaacgaatctgttactt 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 10.0%; Score 28.2; DB 4; Length 1414; Best Local Similarity 57.3%; Pred. No. 0.78; Matches 51; Conservative 0; Mismatches 38; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 10.7%; Score 30; DB 4; Length 2272; Best Local Similarity 59.3%; Pred. No. 0.2; Matches 51; Conservative 0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cochran, Mark D.
APPLICANT: Unikar, David B.
APPLICANT: Unikar, David B.
TILE OF INVENTION: Recombinant Swinepox Virus
FILE REFERENCE: 39119-H/JML
CURRENT APPLICATION UNIBER: US/08/686,968C
NUMBER OF SEQ ID NOS: 231
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                                                                                                                                        PCT/EP93/00350
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; Patent No. 6221361
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252 ccccgcggctccccaacctctgctaa 277
                                                                                                                                                                                                                           REGISTRATION NUMBER: 36.105
REFERENCE/DOCKET NUMBER: 9564-
TELECHOMUICATION INFORMATION:
TELEPHONE: 202/638-5000
FELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2272 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: CDNA from mRNA
US-09-054-5268-2
                                                                                    FILING DATE: 12 FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/F
FILING DATE: 12 FEB-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                              NAME: KITTS, MONICA CHIN REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Ver. 2.1
                   FILING DATE: 01-JUL-1
PRIOR APPLICATION DATA:
APPLICATION NUMBER: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Swinepox virus
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (1)..(1407)
US-08-686-968C-228
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US-08-686-968C-228
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TITLE OF INVENTION: Cells and Uses Thereof
                                                                                                                                                                                                                    COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Win
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 2202 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                609-520-3259
                                                                                                                                                                                                   Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                   STREET: 99/ LU.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: linear
US-09-020-753-2
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CITY: Princeton
STATE: NJ
                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
                                                                                                                                      USA
                                                                                                                                                         08543
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                                                                                                                                      COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08655836
Fatent No. 5824486
GENERAL INFORMATION:
APPLICAMT: Borden, Laurence A.
APPLICAMT: Borden, Michael
APPLICAMT: Yokoyama, Midoril
APPLICAMT: Yokoyama, Midoril
APPLICAMT: Albert, Vivian R.
TITLE OF INVENTION: GLYCINE TRANSPORTER-TRANSFECTED CELLS
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: Princeton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 27.4; DB 1; Length 2202;
Pred. No. 2;
0; Mismatches 66; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIble
COMPUTER: TBM PC COMPATIble
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Partenting Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/655,836
FILING DATE: 31-MAY-1996
CLASSIFTCATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: BLOOM, Allen
REGISTRATION NUMBER: 29135
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Patent No. 5968823
GENERAL INFORMATION:
APPLICANT: Borden, Laurence A.
APPLICANT: Tokoyama, Midori
APPLICANT: Albert, Vivian R.
TITLE OF INVENTION: Glycine Transporter-Transfected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 317743-105
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEPHONE: 609-520-3259
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 50.44
Matches 67; Conservative
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US-08-655-836-2
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                             US-08-655-836-2/c
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                                                                                                                                                                                                                                                                                                                                        STATE:
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120 ggagaagaagccgcaagcctctatctaccgtccatttgtttttgcgcgatcggacggct 179
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NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
Dechert Frice & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: DOS
SOFTWARE: ESESEG for Windows Version 2.0
SUSRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    317743-105
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ADDRESSEE: Dechert Price & Rhoads
STREET: P.O. Box 5218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/655,836
FILING DATE: 31-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Patent No. 5824486
GENERL INFORMATION:
APPLICANT: Borden, Laurence A.
APPLICANT: Yokoyama, Midori
APPLICANT: Yokoyama, Midori
APPLICANT: Albert, Vivian R.
TITLE OF INVENTION: GLYCINE TRANSF
TITLE OF INVENTION: AND USES THERE
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APPLICANT: Borden, Michael
APPLICANT: Tokoyama, Midori
APPLICANT: Yokoyama, Midori
APPLICANT: Albert, Vivian R.
TITLE OF INVENTION: Glycine Transporter-Transfected
TITLE OF INVENTION: Cells and Uses Thereof
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIble
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patenting Release #1.0, Version #1.25
CURRENT APPLICATION UNDER: US/08/655,836
FILING DATE: 31-MAY-1996
CLASSIFICATION: 436
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FastSEQ for Windows Version 2.0
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                                                                                                                                                                         ATTORNEY AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION UNDRER: 29135
REFERENCE/DOOKET NUMBER: 31774
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEPHONE: 609-520-3259
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2364 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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MEDIUM TYPE: Diskette
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CLASSIFICATION:
PRIOR APPLICATION DATA:
COMPUTER READABLE FORM:
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120 ggagaagaaagccgcaagcctctatctaccgtccatttgttttgcgcgatcggacggct 179
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0
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                                                               NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: 317743-105
TELECOMMUNICATION INFORMATION:
TELECOMMUNIC. 609-520-3214
TELEFAX: 609-520-3259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: June 19, 2002, 16:32:51 Job time: 16429 sec
APPLICATION NUMBER: 08/655,836
FILING DATE: 31-MAY-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2364 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 ggctagtattacc 252
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US-09-020-753-3
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1: em\_estba:\*
2: em\_esthum:\*
3: em\_esthum:\*
4: em\_estmu:\*
5: em\_estv:\*
6: em\_estp:\*
7: em\_estro:\*
8: em\_htc:\*
10: 9D\_est:\*
11: 9D\_htc:\*
12: 9D\_htc:\*
13: em\_gss\_hum:\*
14: em\_gss\_lnv:\*
15: em\_gss\_lnv:\*
16: em\_gss\_lnv:\*
16: em\_gss\_lnv:\*
16: em\_gss\_lnv:\*

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

EST:\*

Database :

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	AL667528 AL667528	AL067144 Drosophil	BB610652 BB610652	AZ339575 1M0071B12	AV763886 AV763886	A0459250 HS 5078 A	BH437599 BOHAW63TF	AA221432 my22e11.r	AL259384 Tetraodon	AK010602 Mus muscu	AW450316 UI-H-BI3-	C79787 C79787 Mous	BE246832 TCBAP1E51	AI205836 qq33f11.x	AA834925 a 39a02.s	AI016082 ov26910.x	AA889602 ak28d03.s
SUMMARIES	QI	AL667528	CNSOODBS	BB610652	AZ339575	AV763886	AQ459250	BH437599	AA221432	CNS03T4V	AK010602	AW450316	C79787	BE246832	A1205836	AA834925	AI016082	AA889602
	DB	6	12	σ	12	6	12	12	6	12	11	6	10	10	5	6	6	6
	Query Match Length DB	868	1101	1030	644	762	977	668	629	1037	1210	533	578	335	358	410	416	424
æ	Query Match	12.2	12.1	11.8	11.7	11.7	11.7	11.7	11.6	11.4	11.4	11.3	11.3	11.2	11.2	11.2	11.2	11.2
	Score	34.4	34	33.2	33	33	33	32.8	32.6	32	32	31.8	31.8	31.6	31.6	31.6	31.4	31.4
	Result No.	1	c 0	G 3	C 4	2	9	c 2	œ	6	10	11	c 12	c 13	14	15	16	17

c 18 c 19 20	31.2 31.2 31.2	11.11	297 299 391		BB295841 BB285126 AW037599	BB295841 BB295841 BB285126 BB285126 AW037599 EST279057
21 22 23 24	31.2 31 31 31 31	11.1	617 298 620 625	12 12 12	BH087127 AW014292 BH540957 AO874985	RPCI-24 UI-H-BIO BOGYO29
c 25 c 26 27	9 1 1 1 1 1	11.	692 694 768	12	AG145182 BH451673 AL666434	AG145182 Pan trog1 BH451673 BOHEL32TR AL666434 AL666434
28 29 30	30.8 30.8 30.8		440 533 713	10 10 10	AA438686 BJ198148 BI552821	A4436686 LD13013.5 BJ198148 BJ198148 BI552821 603198003
31 c 32 33	30.8		875 918 1101	10	BE962362 BE378992 CNS001C3	BE962362 601655633 BE378992 601236245 AL060188 Drosophil
0 8 8 8 8 8 8	30.6	10.	319	9 6 5	AV308279 AV104431	AV308279 AV308279 AV104431 AV104431
37.03	30.4	10.0	260	100	AI336966	A1336966 4X82b10.X
39 40	30.4	10.	260 289	, , ,	A1537129 A1624907 A1825120	A133/129 qx83a11.x A1624907 ts72g07.x A1825120 wb04q06.x
C 41	30.4	100.0	340 373 389	12	AA051125 AZ812694 AZ510706	AA051125 mg74d04.r AZ812694 2M0079K03 AZ510706 1M0355D23
	30.4	10.	633 795	15	AV689499 AQ876011	AV689499 AV689499 AQ876011 V132B5 mT
					ALIGNMENTS	
RESULT 1 AL667528 LOCUS DEFINITION		AL667528 AL667528 di	7528 7528 directional	la]	898 bp larval cDNA	mRNA linear EST 11-JAN-2002 library Ciona intestinalis CDNA
ACCESSION VERSION KEYWORDS		cione 02026 AL667528 AL667528.1 EST.	GI:181	344	mkna sequence. 34435	
SOURCE ORGANISM	_	Ciona intes Ciona intes Eukaryota;	intestinalis intestinalis ota; Metazoa	٠	Chordata; Urochordata	ordata; Ascidiacea; Enterogona;
REFERENCE AUTHORS		Phlebobranchia; Cionidae; 1 (bases 1 to 898) Genoscope.	hia; Ci to 898	oni ()	dae; Ciona.	
TITLE JOURNAL COMMENT		Ciona intestinalis Unpublished (2002) Contact: Genoscope	tinalis (2002) noscope	di	irectional larval	al cDNA library
		noscope 191 9100 ail: segr PORTANT:	Centre 6 EVRY ef@geno this se	Na ced sco	Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: segref@genoscope.cns.fr, Web : www IMPORTANT: this sequence may contain erro	www.genc
	CDI Dil	Inbrary ironbNAS from Directional Stazione A.	y from which the cifrom bacteria or ot ional larval cDNA l	a co Rap	e cione was isolated r other Eukarya. NA library originate les, Italy, and was p	ited may be contaminated ate from Dr.M.Branno, as prepared in
FEATURES Sourc	υ Θ	luescripta Loc 1. /or /db	plzsk+. Location/Qualifi 1898 /organism="Ciona /db_xref="taxon: /clone="0202G05"	'Qua  ="C  *ta	<pre>iptLSKF Location/Qualifiers 1. 898 /organism="Ciona intestinalis /db_xref="taxon:7719" /clone="02020505"</pre>	i.s."
BASE COUNT ORIGIN	E	/c /n 289 a	lone_li ote="Ve 186 c	.b=" cto	directional larval r: pBluescript2SK+ 157 g 265 t	larval cDNA library" pt2SK+" 5 t 1 others
Query Ma Best Loc Matches	atch cal 5	E	12.2%; ilarity 60.9%; Conservative		Score 34.4; DB Pred. No. 1.5; 0; Mismatches	DB 9; Length 898; ; 36; Indels 0; Gaps 0;
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cDNA clone 2310065E04 5', mRNA sequence.
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                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
JOURNAL
                                     ACCESSION
                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                            AUTHORS
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                                                                                         KEYWORDS
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                                                               VERSION
                                                                                                                   SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr
- Web: www.genoscope.cns.fr)
- Getermination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila malanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswall Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and BST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster genome survey sequence T7 end of BAC # BACR27J14 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
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                                        69 gcagtgcacgcaaccactttccacgtcaccaatccaggtgagtagcttgctggagaagaa 128
                                                                                         298 GTAATACATGAAACAACATTCCACGTCACCAAACGTTGTGAGTATATTGCTTGTGCAATG 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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41.7%; Pred. No. 2.3;
tive 23; Mismatches 47; Indels (
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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                                                                                                                                                                                                  358 IGCAIGTAAGCGCTIGGAACAGCTCAGCTGTT 389
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/note="end : T7"
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KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
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linear EST 31-AUG-2001

BB610652 RIKEN full-length enriched, adult male tongue Mus musculus

mRNA

1030 bp

BB610652

DEFINITION BB610652/c

RESULT

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Rakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Satio, R., Satio, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., RIKEN Mouse ESTS (Arakawa, T., et al. 2001)

AL Unpublished (2001)

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
The Subhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Yamanaka, I., Kiyosawa, H., Kondo, S., Saito, T., Shinagawa, A., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K., Arakawa, T., Ishi, Y. and Hayashizaki, Y.
Mapping of 19032 mouse cDNAs on mouse chromosomes. J. Struct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              primed with a primer [5, Condition of the primer of the primer of the prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand obna was prepared with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="2310065E04"
/clone_lib="RIKEN full-length enriched, adult male tongue"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genome-resigns.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninci.p., Shibata,Y., Hayatsu,N., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system-384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contributed to prepare mouse tissues. 1st strand cDNA was
                                                                                                                                                            Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /nat_nost__ste__ste__ste__ste__step. Sati; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Func. Genomics 2 pre, L72-L86 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Computer-based methods for the mouse full-length cDNA
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/dev_stage="adult"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                              BB610652.1 GI:15391619
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                                                                                                                         house mouse.
BB61065
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSS 29-SEP-2000
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Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Aslam, M., Longarce, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly M., Rose, M., Rose, M., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ339575 644 bp DNA linear GSS 29-SEP-200
1M0071B12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-" /note="Vector: PWD42nv; Puified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
186 atctggcgccaaaaacctctgctaagtccgtgctaagtataaatagccgcgggggctag 245
                                                                                                                                                                                                                                                                                                                                    475 AGCTGAAAGCCCAGAATTCAACTGAGTCTGGTGAATAGTATACATATTCGCGGGACCATG 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                   0;
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                                                                                                                                                                     Score 33.2; DB 9; Length 1030;
Pred. No. 4.1;
0; Mismatches 33; Indels 0
                                                                           1 others
                                                was cleaved with XhoI and SstI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone UUGC1M0071B12 F, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plate: 0071 row: B column: 12
Seg primer: CGTTGTAAAACGACGGCCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 644.
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/clone="UUGC1M0071B12"
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                                                                                                                                                                                                                                                                                                                                                                                                                   415 TATTCCCTCGACTGTTCCCCAGCCAC 390
                                                                                                                                                                                                                                                                                                                                                                                        246 tattaccccgcgggttccccaacctc 271
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AZ339575.1 GI:10413972
                                                                                                                                                                               11.8%;
61.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Class: plasmid ends
                                                                                                                                                                               Query Match 11.8'
Best Local Similarity 61.6'
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606
Fax: 801 585 7177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          house mouse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
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ORIGIN
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AZ339575/C
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SOURCE
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electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for amplicillin resistance."
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Gu,J., Zhao,M., Huang,Q., Xu,X., Li,Y., Peng,Y., Song,H., Xiao,H.,
Gu,Y., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng
Li, Xu,S., Gao,G., Zhang,Z., Tia,J., Fu,G., Ren,S., Zhong,M., Lu,G.,
Yang Y., Gao,G., Zhang,Q., Chen,S., Han,Z. and Chen,Z.
Unpublished (2000)

Contact: Zeguang Han
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              762 bp mRNA linear EST 19-OCT-20 AV763886 MDS Homo sapiens cDNA clone MDSEEE03 5', mRNA sequence. AV763886 AV763886.1 GI:10921734 EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chinese Natíonaí Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pTriplEx2; Site_1: sfiIA; Site_2: sfiIB" 172 c 177 g 209 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Bone marrow"
/cell_type="CD34+ hematopoietic stem/progenitor cell"
/lab_host="BM25.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58 ttactttgcttgcagtgcacgcaaccactttccacgtcaccaatccaggtgagtagcttg 117
                                                                                                                                                                                                                                                                                                                                                                                                       354 ITTCIGIGCACIGAGIGIAGGITATCICIGICCICCTIACAAGCCIAAGGCATICICIGG 295
                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 catttggataagaacgaatctgttactttgcttgcagtgcacgcaaccactttccacgtc 95
                                                                                                                                                                                                                                                                       Score 33; DB 12; Length 644;
Pred. No. 4.1;
0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11.7%; Score 33; DB 9; Length 762; 48.9%; Pred. No. 4.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 ctggagaagaagccgcaagcctctatct 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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/clone_lib="MDS"
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60.7%;
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1 (bases 1 to 977)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites" 6 others
                                                                                                                                                                                                                      GSS 23-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                              AQ459250 977 bp DNA linear GSS 23-APR-1
HS_5078_A1_H03_SP6E RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=654 Col=5 Row=0, DNA sequence.
  Sequence-tagged connectors: A sequence approach to mapping and
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                                                                                                 531 ACCTTCGCTGGATTCTAAATGGGGTATATTGCAAACTGCAGCTTTCCATTTATGGCATTT
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Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
99380589
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/clone_lib="RPCI-11 Human Male BAC Library"
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High Throughput Sequencing Center
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/db_xref="taxon:9606"
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GSS 12-DEC-2001
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1 (bases 1 to 668)

Town,C.D., Van Aken,S., Utterback,T: and Fraser,C.M. Whole genome shotgun sequencing of Brassica oleracea (10published (2001))
Other_GSSS: BOHAW63TR
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 659)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: If
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                  9712 Medical Center Drive, Rockville, MD 20850, USA
  linear
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/organism="Brassica oleracea"
/strain="TO1000DH3"
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668 bp
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                                                                                       BH437599.1 GI:17623320
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schallenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3']; double-stranded cDNA was ligated to Eco RI adaptors (FGTGGATTGGATTGGTACC), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library constructed by Bob Barstead."
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tetraodontidae; Tetraodon.

1 (bases 1 to 1037)

Roest-Crollius H. Jaillon.O., Dasilva.C., Fizames.C., Fisher.C.,
Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
                                                                                                                                                                                                                                                                                           This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 gcagtgcacgcaaccactttccacgtcaccaatccaggtgagtagcttgctggagaagaa 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 GCAGAGGCCCCCAACAGCTGTCCTCATCGCCACCACCGCTTCCTCACTCCATGAG 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:696620"
/clone_lib="Barstead mouse pooled organs MPLRB4"
                                                                                                                                                                                                        4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.6%; Score 32.6; DB 9; Length 659; 60.9%; Pred. No. 5.6;
tive 0; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34; Indels
                                                                                                                                            Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                   Seg primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 472.
Location/Qualifiers
1. .659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="pooled organs"
/dev_stage="7 day"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1037 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 agccgcaagcctctatctaccgtccat 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 AGCCCCTCTTCCTGCTGTTCAT 109
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GSS; genome survey sequence.
Tetraodon nigroviridis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="FVB/N"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53; Conservative
                                                                                                                             Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 53; Conserva
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ORIGIN
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AUTHORS
                                                                                                     TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
CNS03T4V
    AUTHORS
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KEYWORDS
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Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus ES cells cDNA, RIKEN full-length enriched library, clone:2410027J01:homolog to NICOTINATE-NUCLEOTIDE PYROPHOSPHORYLASE [CARBOXYLATING] (EC 2, 4.2.19) (QUINOLINATE PHOSPHORYLASE PHOSPHORIBOSYLTRANSFERASE [DECARBOXYLATING]) (QAPRTASE), full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                       Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                          Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
Weissenbach,J. Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 actttgcttgcagtgcacgcaaccactttccacgtcaccaatccaggtgagtagcttgct 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 ATTTTGTTGGGAATTGAATTGTTTATTCAGCATGTGCAAACTGGACATTTGTAGATTTAA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 ggagaagaagccgcaagcctctatctaccgtccatttgtttttgcgcgatcggacggct 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 gagttgatctggcgccaaaaacctctgctaagtcccgtgctaagtataaatagccgcggg 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229 GAGATGGTCCGCCCCTAGTGGCCAAAGGTAGTACTGTAGCAAAATGTTAATACTCATGGT 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="G"
/note="Genoscope sequence ID : C0BG056AC01SPl~end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   169 TAGGTTAAAAAAAAGCATTATTTCCCTACTTTACCTTTGATTTTGTTGCATTTGATAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1037;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 others
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/db_xref="taxon:99883"
/clone="056E01"
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 11.4%;
Best Local Similarity 47.5%;
Matches 95; Conservative
                                                                                                              (bases 1 to 1037)
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Mus musculus
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/clone="2410027J01"

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source
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                                                                                                                                        Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shibata, K. Itoh, M., Alzawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Mishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yonaca, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Division of Experimental Animal Research in Riken contributed to prepare mouse Lissues. First strand cDNA was primed with a primer [5. GAGAGAGAAGAACACTTTTTTTTTTTTTTTTTTTT 3.], DNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. CDNA went through one round of normalization to Rot = 5.0 and subtraction to Rot = 25.0. Second strand cDNA was prepared with the primer adapter
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Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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The RIKEN Genome Exploration Research Group Phase II Team and the
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Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Please visit our web site (http://genome.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5 (bases 1 to 1210)
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MEDLINE
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REFERENCE
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sednence (2,

/db\_xref="MGD:MGI:1896569" /db\_xref="taxon:10090" /organism="Mus musculus" Location/Qualifiers

/strain="C57BL/6J"

source

FEATURES

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/clone_lbs="NCL_CGAP_Sub5"
/clone_lbs="NCL_CGAP_Sub5"
/lab_host="DH10B (Life Technologies)"
/lab_host="DH10B (Life Technologies)"
/lab_host="NetCI: Site_1: Bco RI; NCI_CGAP_Sub5
polylinker; Site_1: Not I; Site_2: Eco RI; NCI_CGAP_Sub5
is a subtracted library derived from NCI_CGAP_Sub4. The
NCI_CGAP_Sub5 library had 3 million recombinants. A
single-stranded DNA preparation of NCI_CGAP_Sub4 was used
as a tracer in a subtractive hybridization with a driver
comprising: the IMAGE pool (NCI_CGAP_Kid3 pool 1 LLAM
334-337, 3682-3683, 3798-3803 (IMAGE CloneIDS
1322376-1323911, 1456008-1456775,1500552-1502855);
NCI_CGAP_Kid5 pool 1 LLAM 338-3342,3722-3725,
(IMAGE CloneIDS 1323912-1325831, 1471368-1472903,
1492104-1493255); NCI_CGAP_Lu5 pool 1 LLAM 3575-3582,
3851-3854 (IMAGE CloneIDS 1414920-1417991,1520904-1522439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nlh.gov
The sequence contained an oligo-dr track that was present in the oligonucleotide that was used to prime the synthesis of first strand chan and therefore this may represent a bonafide poly A tail. cDNA and therefore this may represent a bonafide poly A tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution: NIT-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
Www-bio.llnl.gov/Dbrp/Image/image.html
/cell_type="ES cells"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                   /note="data source:SPTR, source key:Q15274, evidence:ISS homolog to NICOTINATE-NUCLEOTIDE PYROPHOSPHOSYLASE [CARBOXYLATING] (EC 2.4.2.19) (QUINOLINATE PHOSPHORIBOSYLKANSFERASE [DECARBOXYLATING]) (QAPRTASE)" 334 c 359 g 264 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 533) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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UI-H-BI3-akz-h-03-0-UI.sl NCI_CGAP_Sub5 Homo sapiens cDNA clone IMAGE:2736221 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                              DB 11; Length 1210;
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                                                                                                                                                                                                                                                                                                                                                                                           11.4%; Score 32; DB 1
58.3%; Pred. No. 11;
tive 0; Mismatches
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/clone="IMAGE:2736221"
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Best Local Similarity 58.37
Matches 56; Conservative
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Unpublished (1997)
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); NCI_CGAP_GC4 pool 1 LLAM 3164-3167, 3716-3720, 3733-3735 (IMAGE CloneIDS 1257096-1258631,1469064-1470983, 1475622-1475743); NCI_CGAP_PT22 pool 1 LLAM 4457-2459, 2758-2759, 3062-3068 (IMAGE CloneIDS 985608-986759 pool 1 LLAM 4457-2459, 1101192-1101959, 1217928-1220615); NCI_CGAP_CO10 pool 1 LLAM 544-2653, 2871-2872 (IMAGE CloneIDS 1057416-1061255, 1144584-1145351). (10% of the driver population), plus a pool of 3,840 arrayed clones from NCI_CGAP_Sub1 (IMAGE CloneIDS 2708616-2710535) and NCI_CGAP_Sub1 (IMAGE CloneIDS 2708616-2710535) (10% of the driver population), plus a pool of 11,136 clones from NCI_CGAP_Sub3 (IMAGE CloneIDS 2712455) (10% of the driver population), plus a pool of 11,136 clones from NCI_CGAP_Sub3 (IMAGE CloneIDS 272245959)) (10% of the driver population), subtraction was performed as previously described (Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 578)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Doi Bloasymmetry Project, ERATO
Japan Science and Technology Corporation (JST)
WBG Marive East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan
Email: hdebioa, jst.go.jp.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C79787 578 bp mRNA linear EST 26-JT C79787 Mouse 3.5-dpc blastocyst CDNA Mus musculus CDNA clone
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/clone="J0071H05"
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Best Local Similarity
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C79787/c
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/clone\_lib="Mouse 3.5-dpc blastocyst cDNA"

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/note="Vector: lambda pSB; Site_1: BamHI; Site_2: EcoRI; First strand cDNA was primed with an anchored Khor-oligo(dT) primer [5'GGAGGACTCGAGGGGCGCGGGGGGGGGG(T)VN Xhor-oligo(dT) primer [5'GGAGCACTCGAGCGCCCCGGGGGGGGGG(T)VN 3'; V=A,C,G; N=A,C,G,T] and then dG tailed. Second strand was primed with a BamHI-dC primer [5'AGAGGCTCGGATCGGGCCGCAATAATAATAATAAT(C) 3']. Double-stranded cDNA was then digested with BamHI and XhoI bouble-stranded cDNA was then digested with BamHI and XhoI and directionally cloned into the BamHI and SalI sites of lambda pSB vector. Library went through one round of normalization. Library was constructed by Wei Yu at RIKEN of Japan (Carninci) P, Westover A, Nishiyama Y, Ohsumi T, Itoh M, Nagaoka S, SasakiN, Okazaki Y, Muramatsu M, Schneider C, Hayashizaki Y, High efficiency selection of full-length cDNA by improved biotinylated cap trapper.,
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA linear EST 03-OCT-2001
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Wei,Y., Tsang,Y.T.M., Mei,G., Ku,J.M., Ali-Osman Jr.,F.R., Muzny,D., Bouck,J., Gibbs,R.A. and Margolin,J.F.
Pediatric Leukemia cDNA Sequencing Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2000)
Contact: Dr. Judith F. Margolin
Texas Children's Cancer Center and Human Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BE246832 335 bp mRNA linear EST 03-OCT-2C TCBAPLE5158 Pediatric pre-B cell acute lymphoblastic leukemia Baylor-HGSC project=TCBA Homo sapiens cDNA clone TCBAP5158, mRNA
                                                                                                                                                                                                                                                                                     65 gettgeagtgeaegeaaceaettteeaegteaeeaateeaggtgagtagettgetggaga 124
                                                                                                                                                                                                                                                                                                                                          430 GCTGGCCTTGCTAGCACACACCONTTTCCCTCACCTGTACTAGAGCTTGGCTTGAGGAAGG 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="TCBAP5158"
/clone_lib="Pediatric pre-B cell acute lymphoblastic
                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                               125 agaaagccgcaagcctctatctaccgtccatttgtttttgcgcgatcggacggctg 180
                                                                                                                                                                                                                                                                                                                                                                                                                               370 ATGAAGGAGCCAGCCTTCTGTTACTAGAAAAATGTTTGGGTTCACACGTGGTGCTG 315
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                                                                                                                                                                        Length 578;
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1102 Bates, MC3-3320 Houston, TX 77030, USA
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                                                                                                                                                                        DB 10;
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/cell_type="pre-B cell"
/dev_stage="pediatric 2 years"
/lab_host="DH10B"
                                                             ų
                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                     Score 31.8; Pred. No. 10;
/tissue_type="blastocyst"
/dev_stage="3.5-dpc"
134 c 113 q 158

    .335
    /organism="Homo sapiens"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE246832.1 GI:9098582
                                                                                                                                                                        11.3%;
54.3%;
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                                                                                                                                                                          Query Match 11.39
Best Local Similarity 54.39
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 832-824-4536
Fax: 832-825-4038
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Length 358;

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Best Local Similarity
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Best Local Simi
Matches 73;
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AA834925
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequencing Center
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 358)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                               245 TITGGCCIGCAGITGITCACIGACIIIGITACCAAIGICCCCAAGAGCIGITCIIGGCCI 186
                                                                                                                                                                                                           185 CAGTCCGGGCTTGGAGGTTGCAGCAGGGCCGTAGGCCCGCGCGTTTGCGCCTGCCATGTT 126
                                                                                                                   Gaps
                                                                                                                                              38 tttggataagaacgaatctgttactttgcttgcagtgcacgcaaccactttccacgtcac 97
                                                                                                                   ;
0
                                                                                    Length 335;
                                                                                                                                                                                                                                                                            158 gtttttgcgcgatcggacggctgagttgatctggcgccaaaaacctctg 206
                  3 others
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                                                                                                                   Indels
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 666 Std Bror: 0.00
Seg Primer: 40UP from Gibco
High quality sequence stop: 288.
Feb 28, 1997)"
                                                                                                                87;
                                                                                    DB 10;
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/sex="male"
                                                                                 Score 31.6; DB
Pred. No. 9.5;
0; Mismatches
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/db_xref="taxon:9606"
/clone="IMAGE:1837005"
 Res 4: 1, 61-6,
88 c 90 g
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                                                                                 11.2%;
48.5%;
                                                                              Query Match 11.27
Best Local Similarity 48.57
Matches 82; Conservative
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Unpublished (1997)
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AI205836
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AI205836
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CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1694 Std Error: 0.00
Seq primer: -40ml3 fwd.ET from Amersham
High quality sequence stop: 357.
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O
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
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                                                                                                                                                                                                                                                                                                                              410 bp mRNA linear EST 31-DEC-1998 aj39a02.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1392650 AA834925
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                      Gaps
                                                                                              33 ttccatttggataagaacgaatctgttactttgcttgcagtgcacgcaaccactttccac 92
                                                                                                                                             1 TTTTTTTGGGGAAGAATGTGTCATTTTCTGAATCCCTTCTCCACTGACCCACTTTCCAT 60
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                                                                                                                                                                                                                     61 CCCTCCACACACATCAGTAGGTTGATGGCTTCTACTGGTCCAGGCCCCT 110
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Score 31.6; DB 9; Length 3
Pred. No. 9.8;
0; Mismatches 49; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:1392650"
/clone_lib="Soares_testis_NHT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert Strausberg, Ph.D.
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/organism="Homo sapiens"
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  11.2%;
55.5%;
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Unpublished (1997)
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- Qy Dp
- 158 gtttttgcgcgatcggacggct 179 | | | | | | | | | | 121 CCTCAGGGACCTTCGGGCCGTT 142
- Qy Db

Search completed: June 19, 2002, 14:04:31 Job time: 7529 sec

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AR172770 Sequence M2963 Coconut fol AP004548 Lotus jap AX036735 Sequence X2938 Commelina y 281038 Caenorhabdi

AL13578C AGRICAL ALLO86632 Human DNA AC108955 Human DNA AC1089771 Homo sapi AC018764 Homo sapi AC018764 Homo sapi AC01859 Homo sapi AC08990 Homo sapi AC08990 Homo sapi AC08990 Homo sapi AC104068 Homo sapi AC018595 Homo sapi AC018625 Homo sapi AC018626 Homo sapi AC018626 Homo sapi AC018625 Homo sapi AC018626 Homo Sap

Scoring table:

Searched:

Minimum DB Maximum DB

Database

Title: Perfect score:

Sequence:

OM nucleic

Run on:

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1 (bases 1 to 1291)
Rohde, W., Becker, D., Randles, J.W., Hehn, A. and Salamini, F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e of a virus DNA as promoter
lent: US 6303345 A 1 16-OCT-2001;
Location/Qualifiers
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Sequence 1 from patent US 6303345.
AR172770.1 GI:17912261
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AC078825
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AC044882
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AC008990
AC009009
AC104068
AL355350
AC010620
          CFDCG
AP004548
                         AX036735
CYMVCG
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AL135782
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AL139381
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AB040712
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AB040542
AB040714
DROGPDHC
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AL358779
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AC019285
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JOURNAL
FEATURES
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AR172770
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 ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS
                                                      June 19, 2002, 15:49:33 ; Search time 5904.86 Seconds (without alignments) 184.285 Million cell updates/sec
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                                                                                                        1 aataaaagattccatttgga......tgttactttgcttgcagtgc 52
                                                                                                                                                                     3595312
       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                   1797656 segs, 10463268293 residues
                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                         US-09-462-955B-1_COPX_734_785
52
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Maximum Match 100%
Listing first 45 summaries
                                       - nucleic search, using sw model
                                                                                                                        IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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em_htg_inv:*
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ACO44882 Homo sapi ABO40712 Clostridi ABO40712 Clostridi ABO40713 Clostridi ABO40713 Clostridi ABO40714 Clostridi L41647 Drosophila AL670195 Mus muscu AL391356 Homo sapi AL391356 Homan DNA AL395614 Human DNA AL45563 Human DNA

U89127 Sus scrofa AP004093 Oryza sat AC055742 Homo sapi

AC073574 Homo sapi AC019285 Homo sapi AL353741 Human DNA

PAT 17-DEC-2001

Score 52; DB 6; Length 1291; Pred. No. 5.6e-07;

100.0%; 100.0%;

Query Match Best Local Similarity

Description

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Score

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/codon_start=1
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blirnlwnsawrioadfedalytelrwngodgplkirshfhitigslkcclrsesort
iaossgyadeteetgspclpnisbssptgsthvvepprryctstsrtonei"
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DEVRRALILLDVPRCNLEYLNYALLECVKNRAFSSDKYEPLSYLGFBHVHVLVFANVLPD
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                                                                                                                                                                 circular VRL 02-AUG-1993
                                                                                                                                                                                                                                           circular; complete genome.
Coconut foliar decay virus DNA, clones NMORG, pORG, and pORGSAU3A.
Coconut foliar decay virus
                                                                                                                                                                                                                                                                                          Viruses; ssDNA viruses; Nanovirus.

1 (bases 1 to 1291)

Robde,W., Ratolles,J.W., Langridge,P. and Hanold,D.

Nucleotide sequence of a circular single-stranded DNA associated
with coconut foliar decay virus
Virology 176, 648-651 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                  Draft entry and printed sequence for [1] kindly submitted by W.Rhode, 15-WAR-1989, for release after publication. Location/Qualifiers
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                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Coconut foliar decay virus"
/db_xref="taxon:12474"
                                                                                                                                                                   Coconut foliar decay virus, complete genome. M29963
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/note="ORF 5"
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PAT 16-NOV-2000
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/protein_id="AAA42899.1"
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                                                                                                                                                                                                                                                       /clone="Ljr31L24"
/clone_lib="Ljr library"
/note="TM0228b, a part of TAC clone:TM0228"
in 3232 c 3509 g 6214 t
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Pred. No. 5.6e-07;
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/db_xref="taxon:34305"
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Pred. No. 21;
0; Mismatches
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Sequence 1 from Patent WO0058485.
AX036735
AX036735.1 GI:11226244
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80.5%;
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KKLSEEVIVFTPEVKINLRDLAHNIHIIAHRVALGFKVIYLYLVDIIFPLLKNIQKSQ
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WRMRFKDEYONLAKIANQDGGTOAILSQIRRIFLGEDPVLGQNTVQNTAFRKLKGLVC
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TKYTGRAHDHHIRYKAKYQRKCKYICGGGHYANQCRNKHKDQQRVAILQSLDLKE
NEEVVSADDKEREDDEIFSVLGEEDVEETINVLEEDDIGITREFT
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CHCHAVYCFWCAEAYHDVQARKILSKDYSFSARGKKGKAVIIEEDEIEBEELISQUQ
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GENGULOKQVBRLQEELMKLHRRKDAFKASRVFSTLOESDEAELNLIREELRO
FKEETFRAIAQLKEAIIVQEBOTIEBERCAMILEEKHTENIYSATAKAEYNGLYNVKVG
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RSKIYSKFDLKSGFWQVAMEEESVPWTAFLAGNKLYEWLVMPFGLKNAPAIFORKMDN
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ROKMAPTGRKRNPETWKNYRQIKERVKNLPDLGAPROSTIIETDGCMTGWGAVCK
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GWQGEDNLLITRGLTGRLSNTSNVGFAYDVKAMVEHLQSNGVKAIKGEKWDAKRFHNG
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EINHSLNLILNDEESTDEDEEFYQYQYRYAWSQVGDSTFYYDTDGVWEEIDRCNDLPEY
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SRSRSSSASSTSMQDDVEEIVRLMKEMRMKKQKKKKRAQQALSSQAQEEPIIEENIEEN
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GRILLIGEQYFRMPVTYVMNMGLSPGIQMIIGCSFIRSLEGGLRIEKDIITFYKLVTSI
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    .23
/note="put. tRNA-Met (put. primer for minus strand

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/note="3bp deletion in pcoYMV100"
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/codon_start=1
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1098. 1505
/note="ORF 2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="t in clone pCoYMV100"
                                                                                                                                                                                                                                  /codon_start=1
/protein_id="CAA37108.1"
/db_xref="G1:59048"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="CAA37109.1"
/db_xref="G1:59049"
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/db_xref="GI:59050"
                                                  synthesis )"
/product="tRNA-Met"
                                                                                                    300. .302
/note="gac was cga"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                        /note="ORF 1"
                                                                                                                                                         citation=[1]
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Medberry, S.L., Lockhart, B.E. and Olszewski, N.E.
Properties of Commellina yellow mottle virus's complete DNA
sequence, genomic discontinuities and transcript suggest that it is
a pararetrovirus
                                               Synthetic construct artificial sequence.

1 (bases 1 to 243)

Rance,T., Theisen,M. and Gruber,V.

Chimeric expression promoters originating from commelina yellow mottle virus and cassava vein mosaic virus.

Patent: WO 0058485-A 1 05-CCT-2000;

MERISTEM THERAPEUTICS (FR); RANCE IANN (FR); THEISEN MANFRED (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (02-MAY-1990) Olszewski N.E., University of Minnesota, Dept of Plant Biology, 220 Biological Sciences Center, 1445 Gortner Ave., St. Paul, MN 55108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (29-NOV-1990) Olszewski N.E., University of Minnesota, Dept of Plant Biology, 220 Biological Sciences Center, 1445 Gortner Ave., St. Paul, MN 55108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VRL 12-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                              /note="243 bp promoter fragment from the intergenic region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complete genome; protease; reverse transcriptase; ribonuclease H. Gomellina yellow mottle virus. Commellina yellow mottle virus virus viruses; Retroid viruses; Badnavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 243;
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/db_xref="taxon:10653"
/clone="pCoYMV89 (and pCoYMV89)"
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                                                                                                                                                                                                                                                                                                                                                                                                                            Commelina Yellow Mottle Virus"
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Pred. No. 1.2e+02;
0; Mismatches 16;

    .243
    /organism="synthetic construct"
    /db_xref="taxon:32630"

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69.2%;
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2 (bases 1 to 7489)
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Olszewski, N.E.
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Olszewski, N.E.
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Submitted (21-OCT-1996) Nematode Sequencing Project, Sanger
Submitted (21-OCT-1996) Nematode Sequencing Project, Sanger
Institute, Hinkton, Cambridge CBIO 1SA, England and Department of
Genetics, Washington University, St. Louis, MO 63110, USA. E-mail:
jes@sanger.ac.uk or rw@enmatode.wustl.edu
Coding sequences below are predicted from computer analysis, using
predictions from Genefinder (P. Green, U. Washington), and other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Current sequence finishing criteria for the C. elegans genome current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CEC25A1 40597 bp DNA linear INV Caenorhabditis elegans cosmid C25A1, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 7489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 26.4; DB 14;
Pred. No. 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 16;
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                                                                                                                     /note="c in clone pCoYMV100"
4611
                                                                                                                                                                  /note="a in clone pCoYMV100" 4794
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6302
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7378
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1389 c 1577 g 1861 t
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Mortimore, B.J.
                                          2672. .2674
/note="ccc was cc in [1]"
                                                                                 /citation=[1]
2977
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CEC25A1/c
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEYWORDS
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δλ

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This sequence is the entire insert of clone C25Al. The true right end of clone F1663 is at 23255 in this sequence. The start of this sequence (1. .104) overlaps with the end of sequence 281065. The end of this sequence (40494. .40597) overlaps with the start of sequence AL032656.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QFALHYSFVDEASARIFLKNAVGMLKPGGVFTGTLPDADRIVWSMRNGENGGFANEVC
KITYENVEELAEGKVPLFGAKFHFSLDEQVNCPEFLAYFPIVKHLLEELDMELLFVHN
FAALINKWIEDEGRRLLESMTGLETYPNEKLSGKSDDEYLEARAKLDAFPEDERIKTMG
TLSKSEMEALCMYLVFGFRKKKSEAEKTEEEPATTKPVAESSESEQKEVTESEEKEDOE
DCEHQEAQTN"
                                                                                                                                                                                                                                                                                                  IMPORTANT: This sequence is NOT necessarily the entire insert of the specified clone. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MMKEVLDAFRKSGEAEGFGHNKMSSSEVASHYNKVLQVGIEGRK
ESRIFFMRNMNNWVKSQLINDAKQRVNDNGVNNPRVLDLACGKGGDLKKWDIAGAKDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VMADVADVSIQQAEERYKQMFGYKKNNIFTVQFIVADCTKENLEDRIENKDPFDLVSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="mSSGFVSTSELDEEKKARQEAWEKIRKPTDATLVPEPEYCNKTL
FEQLKNNKDAKQLEIDEAKKLKNWVRGIDEDESVFLSELDSTKRVVKMRMKREEQELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KELAVTQHLAANQPSSSRFILKPSTSKVLGPPKSKQAAFLSTAIKRKSTSTEEKKQED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVSSKVSKPEPVIKQIGALQALCEYDPSSDSESDASSDDEPETLSLLQTSKSAAQGGC
E"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MSHSKYYIHKVYLCONGKTICLHSSLHILPFTFOLRMEEILROF
LSSSNHSLRDSPFPMIPLSFDTSIMSPTECQOPKPOHSYIGLIAMAILSSPOKKMVLA
EVYEWIMNEYPYFRSRGAGWRNSIRHNLSLNDCFVKAGRAANGKGHYWAVHPACVKDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity to Rat hepatocyte nuclear factor 5 (TR:Q63248), contains similarity to Pfam domain: PF00250 (Fork head domain), Score=170.0, E-value=1.3e-47, N=1"
                                                                                                                                                                                          For a graphical representation of this sequence and its analysis see:- http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .3279,3326. .3424,3471. .3726,3772. .3979)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      jóin(3183. .3279,3326. .3424,3471. .3726,3772. .3979)
/gene="C25A1.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(893. .1316,1650. .1829,1913. .2091, 2159. .2268,2316. .2441,2547. .2677,4012. .4070)) / gene="c25A13" / note="e25A13" / note="predicted using Genefinder Similarity to Yeast ABD1 protein (SW:P32783)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(4537. .4791,5002. .5130,5716. .5920,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(4537. .4791,5002. .5130,5716. .5920,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(join(893. 1316,1650. 1829,1913. 209:
2159. 2268,2316. 2441,2547. 2677,4012. 4070))
/gene="C25A1.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA EST EMBL: T01105 comes from this gene"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Caenorhabditis elegans"
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/db_xref="GI:3874433"
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/db_xref="G1:3874437"
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/db_xref="G1:3874436"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:6239"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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/gene="C25A1.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="C25A1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="C25A1.1
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/gene="C25Al.
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gene

CDS

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M (SW:P52272), Contains similarity to Pfam domain: PF00076 (RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)), Coore=149.2, E-value=2.3e-41, N=3 CORE=149.2, E-value=2.3e-41, N=3 YK103b6.5 comes from this gene; CDNA EST yK103b6.5 comes from this gene; CDNA EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RMVFITUIAYEARWVDLKSLYREKGGEVAFCELLEDRNGKPKGNAVVEFETREGAEKC
VENLQKEDWRGKTILAKEIRDPNAFFETIKTETGIDYLSRFKGGGGGGGGEPPPKDLDR
VERTGCFYDLFGLNMETRQHNIEPPLGERIFIANLAFNVGTOKLYEVEGMAGKITWMD
FRIDKEGKSKGVCVIQYTHPIEAVQAVSMLNGORLFDRNLVVKMDRFDKELEHKEGGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="predicted using Genefinder
Similarity to Human heterogenous nuclear ribonucleoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comes from this gene
cDNA EST yk96b9.3 comes from this gene; cDNA EST yk103b6.3
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grgdfrrrraqrkvrrhmglqvedgdssdeegspgsdpspplfptalwnfncaprap1
                                                                            complement(join(10668. 10859,10913. .11161,11529. .11768,
11817. .11918,12634. .12849,12917. .13203,13283. .13361))
/gene="C25A1.4"
                                                                                                                                                                                                                                                                                         complement(join(10668. 10859,10913. 11161,11529. 11768,
11817. 11918.12634. 12849,12917. 13203,13283. 13361))
/gene="c25A1.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               yk65f12.5 comes from this gene
CDNA EST EMBL:T00718 comes from this gene; cDNA EST
yk51h5.3 comes from this gene
CDNA EST yk82b2.3 comes from this gene; cDNA EST yk84e6.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 comes from this gene CDNA EST yk81b5.5 comes from this gene; cDNA EST yk82b2.5 comes from this gene cDNA EST yk84e6.5 comes from this gene; cDNA EST yk84e6.5 comes
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cDNA EST YK65f12.3 comes from this gene; cDNA EST
yk145b5.5 comes from this gene
cDNA EST yk145b5.3 comes from this gene; cDNA EST
yk26465.3 comes from this gene; cDNA EST
yk216b7.3 comes from this gene; cDNA EST
yk216b7.3 comes from this gene
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7k445b4.3 comes from this gene; cDNA EST
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/k638g7.3 comes from this gene;
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/db_xref="G1:3874432"
/db_xref="SPTREMBL:09XVS2
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yk676a4.5 comes fro
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Join(17983. .18084,18137. .18271,18320. .18423,18471. .18857, 18906. .19063,19304. .19368)
/gene="C25A1.5" 3004. .19368)
Join(17983. .18084,18137. .18271,18320. .18423,18471. .18857, 18906. .19063,13304. .19388)
PRGLESIGMGLGAEGAPLSNVHGMFPGDASVPFTAPAAPFVGGPQVVSAGGFGGVVEQ
                                               PSDYTWQIVRDRVRNFGEVDSVDMMAPGAARIRFATFQDAERARAALYGSTVEGRMIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL135782 63682 bp DNA linear HTG 16-NOV-2001 Homo sapiens chromosome X clone RP3-346A12 map q21.1-21.33, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
                       ANFARSVMNNGPFGGNAGVGGAGGATFAQPDVFGVNGAGGLAGAATPQATRVIIIRNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M77815; 8% of reads
Sequencing vector: plasmid: L08752; 91% of reads
Chemistry: Dye-terminator AB1; 13% of reads
Chemistry: Dye-terminator B1g Dye; 45% of reads
Chemistry: Dye-terminator B1g Dye; 45% of reads
Chemistry: Dye-terminator ET-amersham; 40% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dye-primer Big Dye: 1% of reads
Consensus quality: 63600 bases at least 040
Consensus quality: 63636 bases at least 030
Consensus quality: 63661 bases at least 020
Insert size: 65682; sum-of-contigs
Insert size: 112558; 14.7% error; agarose-fp
Ouality coverage: 10.57x in 020 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                       Similarity to Yeast hypothetical 44,9 KD protein (TR:003529) cDNA EST EMBL:T00034 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 3; Length 40597;
                                                                                                                                                                                                                                                                                                                      CDNA EST EMBL:T00034 comes from this gene CDNA EST EMBL:T00035 comes from this gene CDNA EST EMBL:T01495 comes from this gene CDNA EST yk340G7.3 comes from this gene CDNA EST yk340G7.5 comes from this gene CDNA EST yk3238.3 comes from this gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16; Indels
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* This sequence will be replaced
                                                                                                                                                                                                                                                    /note="predicted using Genefinder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coverage: 6.23x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.8%; Score 26.4; DB
69.2%; Pred. No. 75;
Live 0; Mismatches
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Contact: humquery@sanger.ac.uk
------ Project Information
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Best Local Similarity
Matches 36; Conserv
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SOURCE
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                                                                                                                                                                             CDS
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FEATURES

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Direct Submission

AL Submitted (28-07-1997) Chromosome X Project Group

(http://www.sanger.ac.uk/HGF/ChrX/) Sanger Centre, Hinxton,

(http://www.sanger.ac.uk/HGF/ChrX/) Sanger Centre, Hinxton,

Cambridgeshire, CB10 13A, UK. E-mail enquires:

(http://www.sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Apr 8, 1998 this sequence version replaced gi:2578085.

IMPORTAMY: This sequence is the entire insert of clone 321115.

IMPORTAMY: This sequence is the entire insert of clone 321115.

Where differences are found these are annotated as variations

Where differences are found these are annotated as variations annotated may not be found in the sequence submission corresponding to the overlapping clone as we submit sequences with only a small overlap as described above.

This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre chromosome X mapping group. Further information can be found at http://www.sanger.ac.uk/HGP/ChrX/

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the feature be.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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The true left end of clone 321115 is at 1 in this sequence. The true right end of clone 321115 is at 75793.

321115 is from the library Rec11 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong.

For further details see http://bacpac.med.buffalo.edu/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HS321115 75793 bp DNA linear PRI Human DNA sequence from PAC 321115 on chromosome Xq21.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                           Length 63682;
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 26.4; DB 2; Length 6 Pred. No. 72; 0; Mismatches 11; Indels
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                                                                                                                                                                                                                                                                                              /note="assembly_fragment:00926"
11146 c 11344 g 20582 t
                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="x"
/map="q21.1-21.33"
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/db_xref="taxon:9606"
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/clone_lib="RPCI-3"
1. .63682
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/clone="RP1-321115"
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Best Local Similarity
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ORIGIN
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RESULT

HS321115

Matches

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DEFINITION

ACCESSION

KEYWORDS

SOURCE

VERSION

ORGANISM

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

FEATURES

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/note="LTR8 repeat: matches 690. .1 of consensus" 9239. .9272
/note="17" copies of 2 mer 82 % conserved" 9487. .9788
/note="Alusq repeat: matches 1. .302 of consensus" 10895 ..11248
/note="THEIC repeat: matches 370. .1 of consensus" 11987. .12612
/note="LTRE repeat: matches 1. .558 of consensus" 13703 ..14143
                                                                                                                                                                                                                                  /note="MER4A2 repeat: matches 211. .506 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jobbs 14597 Latter matches 611. .194 of consensus" 1453. .14597 Latter matches 219. .1 of consensus" //note="MER4B repeat: matches 219. .1 of consensus" //note="23 copies of 2 mer 89 % conserved" 16825. .16550 //note="AluJo repeat: matches 136. .11 of consensus; incomplete repeat" 18670. .18972
1184. .1696
/note="LiPA5 repeat: matches 378. .892 of consensus"
                                                                                                                                                                                                                                                                                           .450 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 incomplete repeat."
19189. .13340
//note="MRR39 repeat: matches 311. .460 of consensus"
19990. .20292
//note="AluSg repeat: matches 1. .303 of consensus"
21851. .21989
//note="LiPp2 repeat: matches 183. .41 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22141. .22409
/note="LIME3 repeat: matches 911. .635 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23025. ,23532

/note="2 copies of 254 mer 100 % conserved"

23884. ,24289

20026. ,26319

26286. ,26319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="L1 repeat: matches 4372. .5384 of consensus" 34668. .35665
                                                                                                                                                                                    /note="MER4A2 repeat: matches 1. .152 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluJo repeat: matches 302. .1 of consensus" 3087. .30979
/note="FLAM_C repeat: matches 133. .1 of consensus" 30997. .31030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         //note="MLT1A2 repeat: matches 1. .374 of consensus"
33120. .33192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="MER5B repeat: matches 155. .84 of consensus"
33812. .34808
                                                                              /note="AluSq repeat: matches 1. .302 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .1 of consensus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .2 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ante-7. 26955
7. Ante-7. 28531
7. Ante-7. 28531
7. Ante-7. 28531
7. Ante-7. 28531
29316. 29645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="AluJo repeat: matches 301. .2 of consensus 19098. .19184
/note="AluJb repeat: matches 1. .87 of consensus;
                                                                                        /note="17 copies of 2 mer 88 % conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="17 copies of 2 mer 82 % conserved"
32102. .32229
/note="AluJo repeat: matches 129. .1 of or
incomplete repeat"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .81 of
                                                                                                                                                                                                                                                                /note="MER34 repeat: matches 530.
7224. .7954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21851, .21953
/note="L1MD2 repeat: matches 183.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .26319
                                                        .2800
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"note="MST-INTERNAL repeat: matches 1651. .1 of consensus"
19833. .50232
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51475. .51694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MER25 repeat: matches 2135. .1510 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MER25 repeat: matches 1296. .1079 of consensus"
51723. .52016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="MER25 repeat: matches 1057. .602 of consensus"
52672. .53166
                                                                                                                                                                                                                                                                                                                                                                                                                                                  41628. .41914
/note="LIPB3 repeat: matches 896. .591 of consensus"
41746. .42317
/note="LIMA5_repeat: matches 758. .136 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="FLAM_A repeat: matches 128. .11 of consensus" 53875. .54925
/note="THEIB-INTERNAL repeat: matches 107. .1167 of
                                                                                           611. .297 of consensus"
                                                                                                                                                                                                                                               /note="AluJb repeat: matches 166. .301 of consensus;
                                                                                                                                                                                                                                                                                         39884, .40234
/note="MLT1A1 repeat: matches 365, .1 of consensus"
40875, .41053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="L1 repeat: matches 5377. .2924 of consensus"
44915. .45196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45240. .45848
/note="L1 repeat: matches 2875. .2257 of consensus"
45872. .46170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .29 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       // Mote="11 repeat: matches 2198. .1356 of consensus" 47151. .47767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .49 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55252. .56389
/note="L1 repeat: matches 3226. .2078 of consensus"
56380. .56619
/note="L1MB5 repeat: matches 242. .2 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="L1 repeat: matches 5390. .4668 of consensus" 57183. .57486 //note="AluSq repeat: matches 1, .303 of consensus" 57509. .59386
/note="L1MA4 repeat: matches 4. .1046 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54929. .55248
/note="THBIC repeat: matches 54. .368 of consensus"
                                                                                                         38453. .38682
/note="MRR4B repeat: matches 231. .1 of consensus"
39063. .39247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="AluJo repeat: matches 17. .293 of consensus;
                     36335. .36634 / Mote="AluJo repeat: matches 1. .302 of consensus"
                                                                                                                                                                                                                                                                                                                                                        /note="MERSB repeat: matches 1. .173 of consensus" 41288. .41418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anote-"Alujb repeat: matches 5. .302 of consensus" 16258. .46557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="AluSx repeat: matches 297. .1 of consensus"
52028. .52484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="AluJo repeat: matches 300. .1 of consensus"
46572. .47422
                                                                                                                                                                                                                                                                                                                                                                                                              consensus;
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                                                                                                                                                                                                                                                                                                                                                                                                       /note="AluJo repeat: matches 132. .1 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42058. 42427
/note="L1PB2_repeat: matches 395.
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53615. .53733
                                                                                         /note="MER4B repeat: matches
                                                                                                                                                                                                     incomplete repeat"
39702. .39837
                                                                                                                                                                                                                                                               incomplete repeat"
39884. .40234
                                                                                                                                                                                                                                                                                                                                                                                                                                   incomplete repeat"
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                                                                 38448
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Anderson, S., Barna, N., Bastlein, V., Bouklawkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., Dearellano, K., Deark, K.) Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fizzhugh, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Levine, K., Liu, G., MacCanth, M., McEwan, P., McRernan, K., Merquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPheeters, R., Meldrim, J., Menga, V., Murphy, T., Naylor, J., Naylor, J., Maylor, J., Maylor, J., Maylor, J., Maylor, J., Maylor, J., Menga, V., Murphy, T., Naylor, J., Naylor, J., Naylor, J., Maylor, J., O'Connell, P., O'Connell, P., O'Connell, P., O'Connell, P., O'Connell, P., O'Connell, R., Schuback, R., Schauer, S., Schupback, Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tophan, K., Travers, M., Trigilio, J., Ve, W. J., Young, G., Vell, M., Will, M., Wann, J., Vell, M., Wall, M., Wann, J., Vell, M., Wall, Wann, J., Vell, M., Wall, M., Wann, Wann, V., Wassillev, H., Voll, J., Zammer, A., and Zody, M., Ye, W., Vell, J., Young, G., Zainou, J., Zembek, L., Zimmer, A., and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus clone RP24-262D23, LOW-PASS SEQUENCE SAMPLING. AC105955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                 Gaps
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/note="L1 repeat: matches 4680. .2773 of consensus" 39391. .59423
/note="11 copies of 3 mer 85 % conserved" 59435. .59746
                                                                                                                 /note="Alujo repeat: matches 1. .302 of consensus" 29770. .59802 /note="Alusxy repeat: matches 36. .4 of consensus; incomplete repeat"
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0
                                                                                                                                                                                                                                                                       DB 9; Length 75793;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                              Indels
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Mus musculus, clone RP24-262D23
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Web site: http://www-seg.wi.mit.edu
                                                                                                                                                                                                                                                                                                                              0; Mismatches
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Pred. No. 71;
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HTG; HTGS_PHASE0.
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75.0%;
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AUTHORS
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SOURCE
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contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. Will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cont.,
up of 100.
contig of 682 bp 10.
100 bp.
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11004: contig of 691 bp in length
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11813: contig of 709 bp in length
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12715: gap of 100 bp
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June 1, 2001. June 1, 2001. June 1, 2001. June 1, 2001. June 1, 200. J 25 39924: gap of 100 bp o of 100 bp contig of 723 bp in length 37384 37483; gap of 100 bp 37484 38207; contig of 724 bp in length 88208 38307; gap of 100 bp in length in length 34273: gap of 100 bp 34977: contig of 654 bp in length 35067: gap of 100 bp 35762: contig of 695 bp in length 162: gap of 100 bp 1655: contig of 703 bp in length 165: gap of 100 bp 17383: contig of 718 bp in length 17383: contig of 718 bp in length p of 100 bp contig of 688 bp in length 26160: contig of 653 bp in length 42207: Cun-42207: gap of 100 bp 42990: contig of 643 bp in 1 143090: gap of 100 bp 11 43733: contig of 643 bp in 1 100 bp in 100 b 71, 100 bp 77 bp j 100 bp [701 bp 1 100 bp [697 bp 1 100 bp 687 bp 100 bp of 705 bp 47878: gap of 100 bp 48561: contig of 683 bp 48661: gap of 100 bp 49359: contig of 698 bp 100 bp 681 bp contig of 700 bp p of 100 bp contig of 697 bp 51027: gap of 100 bp 51703: contig of 676 bp 51803: gap of 100 bp 52490: contig of 687 bp 27084: contig of 724 bp 27084: gap of 100 bp 27802: contig of 718 bp 350: gap of 100 b 45375: contig of 725 80: gap of 1 46981: contig of contig of contig of contig of 32700: gap of 1 33385: contig of 27902: gap of 1 28619: contig of 45475; gap of 46180; contig con, con, con, sage of 47081: gap of 47778: con gap of 53390: gap of 54113: con gap of gap of 31123: gap of 31924; gap of 33485: gap of 34173: con 213: gap ( 54910: cc , 39125: gar 39824: 50140 50927 46280: 49459: 52590: 50240: 30326: 35862: 28719: 36665: 44650: 54213 29539: 54114 54214 18562 16982 47879 49460 26161 26261 26985 27803 27903 28620 40635 42308 42991 43091 44551 446516181 31825

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/organism="Homo sapiens"
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DOE Joint Genome Institute.
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On Oct 12, 2001 this sequence version replaced gi:15990615.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >-30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one Mi3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; WP:, WORMPEP: Information on the WORMPEP
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RPI1-74A12 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMPORTANT: This sequence is not the entire insert of clone RP11-74A12 It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true left end of clone RP11-46412 is at 114022 in this sequence. The true right end of clone RP11-140119 is at 2000 in
                                                                                                              Gaps
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Human DNA sequence from clone RP11-74A12 on chromosome
13q31.2-32.2, complete sequence.
                                                                                                                                                                                      Db 64983 AATAAAATATTCAATTTTTTAAAAAAAAAATGTTGCTTCAGTTTCTGT 65032
                                                50.0%; Score 26; DB 2; Length 65370; ilarity 70.0%; Pred. No. 96; Conservative 0; Mismatches 15; Indels
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VECTOR: pBACe3.6
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Submitted (03-AUG-1999) Production Sequencing Facility, DOE Joint Secone Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA (Dases 1 to 123169)
DOE Joint Genome Institute and Stanford Human Genome Center.
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/note="Tandem repeat. Forced join. Gap size estimated to be approximately lkb by restriction digest data." 23449\ c 23279\ g 33988\ t
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On Feb 28, 2001 this sequence version replaced gi:7709299.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 123169)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC008771 123169 bp DNA linear PRI 28-FEB
Homo sapiens chromosome 5 clone CTD-2015H6, complete sequence.
AC008771
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                                                                                                                                                                                       49.6%; Score 25.8; DB 9; Length 116021; 73.3%; Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
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                                                                                                                                                                                                                                                        Indels
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Quality: Phrap Quality >-40 99.3% of Sequence;
Estimated Total Number of Errors is 0.9.
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0; Mismatches
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DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE AUTHORS

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JOURNAL REFERENCE AUTHORS

TITLE

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TITLE JOURNAL

REFERENCE AUTHORS JOURNAL

TITLE

COMMENT

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Spiren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barren, B., Linton, L., Nusbaum, C., Landralter, B., Brown, A., Campariano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Campoplano, A., Chepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz., J. S., Godge, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Haros, B., Heaford, A., Lancque, K., Lamazares, R., Landers, T., Lohnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lahders, T., MacLean, C., MacConald, P., Marthews, C., McCarthy, M., McEwan, P., McKernan, K., Marthews, C., McCarthy, M., McEwan, P., McEwan, P., McRernan, K., Marthews, C., McCarthy, M., McEwan, P., Menga, V., Murphy, T., Naylor, J., Moule, L., Mihova, T., Menga, V., Phunkhang, P., Pierre, W., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Strauss, N., Subramanian, A., Taalamas, J., Tesfaye, S., Theodore, J., Strauss, N., Subramanian, A., Taalamas, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Whilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Senbanse, L., Zimmer, A. and Zoddy, M. Direct, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (10-MAR-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Nov 18, 2001 this sequence Version replaced 91:14336507.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center project Information
Center project name: L1284
Center clone name: L024_N.24
Center clone name: 2054_N.24
Assembly program: Phasmid; n/a; 100% of reads
Assembly program: Phasmid; version 0.960731
Censensus quality: 143329 bases at least Q30
Censensus quality: 143488 bases at least Q30
Censensus quality: 143566 bases at least Q20
Insert size: 172000; agarose-fp
Insert size: 143667; sum-of-contigs
Quality coverage: 10.5 in Q20 bases; sum-of-contigs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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/clone_lib="CITD Human BAC"
1. .24723
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/chromosome="15"
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                                                                                             AUTHORS
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143867 bp DNA linear HTG 18-NOV-2001
HOMO sapiens chromosome 15 clone CTD-2054N24 map 15, WORKING DRAFT
SEQUENCE, 3 unordered pieces.
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                            linear PRI 09-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (19-DEC-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
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Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 15, clone CTD-2054N24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (01-UUL-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 126084)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (09-NOV-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA ON Nov 9, 2000 this sequence version replaced gi:8886981.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AC018764 126054 bp DNA linear PRI 09-NON
Homo sapiens chromosome 5 clone CTD-2327L5, complete sequence
AC018764
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Finishing Completed at Stanford Human Genome Center
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Quality: Phrap Quality >=40 99.5% of Sequence;
Estimated Total Number of Errors is 0.5.
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HTG; HTGS_PHASE1; HTGS_FULLTOP.
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Location/Qualifiers
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/db_xref="taxon:9606"
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DOE Joint Genome Institute.
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WI-15051 G23648
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Query Match

Matches

BASE COUNT

ORIGIN

DEFINITION

LOCUS

ACCESSION

VERSION KEYWORDS

RESULT 13 AC090825/c ORGANISM

SOURCE

AUTHORS TITLE

REFERENCE

source

FEATURES

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L (Dasses I to 176476)

Ruzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Banton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Brinage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Brater, M., Cavazos, S.R., Chacko, J., Chavaz, D., Chen, G., Caron, T.E., Carter, M., Cavazos, S.R., Chacko, J., Chavaz, D., Chen, G., Cox, C., Coyle, M. D., Dathorne, S.R., Darid, R., Davila, M.L., Davis, C., Coyle, M. D., Dathorne, S.R., Darid, R., Dathwalte, K.J., Deaper, H., Dugan-Rochs, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhai, C., Esocutch, M., Palls, T., Ferraguco, D., Flago, N., Ford, J., Foster, P., Frantz, P., Galisi, A., Gao, J., Garcia, A., Garner, T., Foster, P., Frantz, P., Galisi, A., Gao, J., Garcia, A., Garner, T., Garzer, M., Galisi, A., Gao, J., Garzia, M., Hullyks, H., Harris, C., Harris, C., Hodes, M., Holloway, C., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Louis, J., Liu, J., Liu, M., Lude, M., Hulyks, Y., Lun, K., Mants, D., Lau, J., Liu, M., Lude, M., Madot, M., Maheshwari, M., Maheshwari, M., Maher, D., Wartin, R., Martin, R., Martin, R., Martin, R., Martin, M., Martin, M., Martin, R., Suter, A., Tabor, P., Tamerisa, R., Tang, H., Tanesy, J., Taylor, C., Taylor, T., Tang, H., Tanesy, J., St
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Rattus norvegicus clone CH230-24H1, *** SEQUENCING IN PROGRESS ***,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                              . Match 49.6%; Score 25.8; DB 2; Length 143867; Local Similarity 73.3%; Pred. No. 1e+02; es 33; Conservative 0; Mismatches 12; Indels 0;
                                                                                                                                                200 others
                                                                                                                                                                                                                                                                                                          le+02;
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* NOTE: Estimated insert size may differ from sequence length
* NoTE: this is a "working draft' sequence. It currently
* norE: This is a "onligs. The true order of the pieces
                      Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced gi:15627714.
                                                                                                                                                                                                                                                                                Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 2.3x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                            Consensus quality: 140728 bases at least Q40 Consensus quality: 150414 bases at least Q30 Consensus quality: 157122 bases at least Q30 Estimated insert size: 149244; sum-of-contigs estimation
                                                                                                                                                                                                   Assembly program: Phrap; version 0.990329First call to
                                                                                                                                                                                                                                                                                                                                                                        is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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                                                                                                                                              Project Information
                                                                                                                               Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                          Center clone name: CH230-24H1
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E Joases 1 to 179762)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Bladwin, J., Barna, N., Beckerly, R., Boquisavki, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., Fizhugh, M., Forrest, C., Funke, R., Gage, D., Hewland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Hein, J., Lehocky, J., Lehu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Feterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Talamas, J., Tasfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wiyman, D., Ye, W. J., Zimmer, A. and Zody, M.

Direct Submission

Research, 320 Charles Street, Cambridge, MA 02141, USA
On Sep 20, 2000 this sequence version replaced gi:9112896.

All repeats were identified using Repeatwasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RW/Repeatwasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                  ACULSOLY 179762 bp DNA linear HTG 20-SEP-2000 Homo sapiens clone RPl1-115014, WORKING DRAFT SEQUENCE, 12 UNDIGGERED pleces.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 179762)
                                                                     Gaps
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Score 25.8; DB 2; Length 176476; Pred. No. 1e+02; 0; Mismatches 12; Indels 0;
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Insert size: 17865; sum-of-contigs
Quality coverage: 6.1 in Q20 bases; agarose-fp
Quality coverage: 5.8 in Q20 bases; sum-of-contigs
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Web site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                               Db 67092 AAAACAATCTIGCATTAGAATAGCAACTAATTTGATACTTTGCTT 67136
                                                                                                                                 1 aataaaagattccatttggataagaacgaatctgttactttgctt 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-115014
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Center clone name: 115_0_14
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      Query Match
Best Local Similarity 73.3%;
Matches 33; Conservative
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* as soon as it is available and the accession number will
* be preserved.
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49.6%; Score 25.8; DB 2; Length 179762;
Best Local Similarity 73.3%; Pred. No. 1e+02;
Matches 33; Conservative 0; Mismatches 12; Indels 0;
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Search completed: June 19, 2002, 15:50:29
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Chimeric expression promoter for transgenic plant production, comprises
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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ABA07740
AAL06924
AAH04923
AAD26402
AAF22305
AAH17538
AAT84527
AAS28623
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Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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                         Human
                                                                                    Human
                                                                                                                                                                                                                                                                                                                                                                                           Promoter; intergenic region; Commelina yellow mottle virus;
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        AAH73180
AAK86765
                            AAT58840
AAH14861
AAQ96127
AAS17049
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AAA97370
AAS60801
AAF16149
AAC01250
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AAH08051
AAI61292
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AAH15133
AAF58337
AAQ85924
AAC61840
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AAK83835
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ABA90193
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ID AAA96835 standard; DNA; 243
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                                                                                                                                                                                                                                                                                                                                                               (first entry)
575
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Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; ds.
                                                                                                            The present sequence represents a promoter fragment from the intergenic region of Commelina yellow mottle virus. The promoter is a strong promoter in vascular and reproductive tissues. The promoter is used to construct chimeric expression promoters. These chimeric promoters comprise a nucleic acid sequence which is derived from a first plant promoter, in which a plant vascular expression promoter region is replaced with a nucleic acid sequence derived from a second plant promoter comprising a plant green tissue expression promoter region. Preferably, the first plant promoter originates from Commelina yellow mottle virus, and the second plant promoter originates from Commelina yellow wein mossic virus. The chimeric promoters are useful for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human ovarian and breast cancer associated polynucleotide SEQ ID NO 535.
sequence from promoter comprising vascular expression region replaced with sequence from promoter comprising green tissue expression region
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                                                                              Claim 4; Page 79; 91pp; English.
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16-MAR-2000;
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02-0CT-2000; 20000S-0237039.
02-0CT-2000; 20000S-0237039.
02-0CT-2000; 20000S-0237040.
13-0CT-2000; 20000S-0239935.
13-0CT-2000; 20000S-0249950.
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20-0CT-2000; 20000S-0241785.
20-0CT-2000; 20000S-0241785.
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(HUMA-) HUMAN GENOME SCI INC

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-488786/53.

New isolated ovarian and/or breast cancer related nucleic acids and polypeptides, useful for diagnosing, treating and/or preventing human diseases and disorders, particularly ovarian and/or breast cancer -

Disclosure; SEQ ID NO 535; 577pp + Sequence Listing; English.

The invention relates to novel genes (ABA07454-ABA08224) and proteins (ABB10743-ABB10980) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are established from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast on ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and parasitic infections.

30-AUG-2000;

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                                                                                                                                                                                                                                                                                  Human; reproductive system related antigen; reproductive system disorder; cancer; gene therapy; ds.
Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                Gaps
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                                                                         Query Match 48.8%; Score 25.4; DB 22; Length 6198; Best Local Similarity 74.4%; Pred. No. 11; Matches 32; Conservative 0; Mismatches 11; Indels 0;
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                                         Sequence 6198 BP; 1979 A; 1100 C; 1215 G; 1904 T; 0 other;
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2000US-0225757
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26-JUL-2000; 2
14-AUG-2000; 2
14-AUG-2000; 2
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18-AUG-2000; 2
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17-MAR-2000;
18-APR-2000;
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07-JUN-2000;
28-JUN-2000;
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2000US-0241785.
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01-SEP-2000;
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05-SEP-2000;
05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
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08-SEP-2000;
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08-SEP-2000;
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14-SEP-2000;
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20-0CT-2000;
20-0CT-2000;
01-NOV-2000;
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21-SEP-2000;
25-SEP-2000;
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02-OCT-2000;
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17-NOV-2000;
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Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides the protein and coding sequences of a number of human reproductive system related antiques. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 9612; 1297pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 6198;
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Pred. No. 11;
0; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                       Rosen CA, Barash SC, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 48.8%;
Best Local Similarity 74.4%;
Matches 32; Conservative (
               2000US-0249214
2000US-0249215
2000US-0249216
2000US-0249218
2000US-0249244
2000US-0249245
2000US-0249265
2000US-0249265
2000US-0249297
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2000US-0250160
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2000US-02501886
2000US-02511868
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2000US-0251990.
2000US-0254097.
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                  17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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01-DEC-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
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05-JAN-2001;
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17-NOV-2000;
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17-NOV-2000;
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08-DEC-2000;
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(GENA-) GENAISSANCE PHARM INC.

18-JUN-2001; 2001WO-US19447. 16-JUN-2000; 2000US-212328P.

WO200196350-A2

20-DEC-2001

Homo sapiens

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of a polynucleotide which comprises one of all gonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprises a 3'-end sequence complementary to the polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primer sets for synthesizing polynucleotides, particularly the 5602 full-length coNas defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length coNas.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Yamamoto J;
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Pred. No. 11;
0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     hikawa T, Hayashi K, Saito K, Ya
Wakamatsu A, Nagai K, Otsuki T;
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                                                                                                                                                                                                                                                                                                                                                                                                                     Isogai T, Nishikawa T,
Sugiyama T, Wakamatsu
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2000JP-0118776.
                                                                     2000EP-0116126.
                                                                                                                                       99JP-0248036
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Best Local Similarity
Matches 31; Conserva
                                                                 28-JUL-2000;
                                                                                                                                                                                                            1-JAN-2000;
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07-FEB-2001
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Ishii S,
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δy QQ 

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The invention relates to an isolated polynucleotide which is a polymorphic variant of glutamate receptor, metabotrophic 3 (RRM3) isogene. GRM3 is a receptor for glutamate, the major excitory neurotransmitter in the mammalian central nervous system. Human GRM3 located on chromosome 7q21.1-q21.2 is expressed in human foetal and adult whole brain especially in the caudate nucleus and corpus collosum. GRM3 DNA is useful in gene therapy and also for studying the expression and function of GRM3. GRM3 polypeptide is used for screening drugs. A recombinant non-human organism is used to study expression of GRM3 great in vivo, for in vivo screening and testing of drugs targetted against GRM3 protein, and for testing the efficacy of therapeutic agents and compounds for neurological disorders in a biological system. GRM3 haplotypes are for treating diseases associated with GRM3 activity, ergone in uncological disorders. The present sequence is human GRM3 gene
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                                                                                                                                                                                                                                                                    receptor, metabotrophic 3 (GRM3) gene for expressing GRM3 protein isoform to screen drugs to treat GRM3 activity-related disease
                                                                                                                                                                                                                                                   New isolated polynucleotide, a polymorphic variant of glutamate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18765 BP; 5932 A; 3526 C; 3474 G; 5833 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana chromosome 4 centromere.
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                                                                                                                                                                                                                                                                                                               Example 1; Fig 3; 165pp; English.
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Best Local Similarity 70.29
Watches 33; Conservative
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                                                                                                                                                                                      Finkel K, Koshy B,
                                                                                                                                                                                                                    WPI; 2002-090198/12
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18-MAY-1999;
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25-OCT-1995;
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AAT84527/c
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                                                                                                                                                      present invention relates to a recombinant DNA construct of a plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                              (Arabidopsis thaliana) centromere. The constructs are useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells expressing selected proteins such as hormones, enzymes, interleukins, clotting factors, cytokines, antibodies, and growth factors.
                                                                                        Recombinant DNA construct comprising a plant centromere, useful for producing stably inherited michrosomes which can serve as vectors for the construction of transgenic plant and animal cells
                                                                                                                                                                                                                          Sequence 1082138 BP; 348775 A; 194404 C; 195515 G; 343444 T; 0 other;
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                                                                                                                                                                                                                                                       47.3%; Score 24.6; DB 21; Length 1082138; 70.2%; Pred. No. 55;
                                                                                                                                                                                                                                                                                                           Saito K, Ya
Otsuki T;
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                                                                                                                                                                                                                                                                                               6 aagattocatttggataagaacgaatctgttactttgcttgcagtgc 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashi K,
                                                                                                                                                                                                                                                                  Pred. No. 55;
0; Mismatches
                                                                                                                                 Claim 68; Page 977-1388; 1449pp; English.
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                                                  Copenhaver G, Keith K;
                                                                                                                                                                                                                                                                                                                                                                    AAH17538 standard; cDNA; 2763 BP
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11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
99US-0153584.
         99US-0154603.
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                                                                                                                                                                                                                                                                            Conservative
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                             UYCH-) UNIV CHICAGO
                                                                                                                                                                                                                                                                Best Local Similarity
Matches 33; Conserva
                                                                     WPI; 2000-587529/55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isoqai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    full-length cDNAs
13-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EP1074617-A2
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          17-SEP-1999;
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                                                  Preuss D,
                                                                                                                                                                                                                                                                                                                                                                                       AAH17538;
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                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                      The
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The present invention describes primer sets for synthesising 5602 full-length cDNas defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the complusional comprises at least 15 nucleotides; where the oligonucleotide which comprises a 3'-end sequence of sequence of in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the proteins encoded by the full-length cDNAs. The primers are also useful for the chill-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the full-length cDNAs. The primers are also useful for the child of the abundant and of the abundant of the full-length cDNAs represent human cDNA sequences; AAH33628 and AAH362893 represent human anino acid sequences; and AAH3629 to AAH3632 crepresent thuman anino acid sequences; and AHH3632 to AAH3632
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22; Length 2763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene signal peptide, prosequence and terminator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pancreatic secretory trypsin inhibitor; enzyme engineering; protein engineering; detergent; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= b
/note= "B. amyloliquefaciens subtilisin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2763 BP; 823 A; 564 C; 635 G; 741 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Subtilisin inhibitor; protease inhibitor; PSTI; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a
"B. subtilis aprE promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46.9%; Score 24.4; DB 73.8%; Pred. No. 23; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric Bacillus subtilis strain BG2036;
Chimeric Bacillus amyloliquefaciens;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmid pBNppt insert.
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14-AUG-2000;
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01-SEP-2000;
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25-SEP-2000;
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27-SEP-2000;
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08-SEP-2000;
08-SEP-2000;
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22-AUG-2000;
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14-AUG-2000;
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23-AUG-2000;
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21-SEP-2000;
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13-OCT-2000;
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                                                                                                                                                                                                          This DNA sequence comprises a DNA insert in vector pBN3 comprising
the Bacillus subtilis aprE promoter and the Bacillus
amyloliquefaciens subtilisin gene signal sequence, pro-sequence and
terminator region (see AAW26365). The vector, pBNppt, can be used
for the expression in B. subtilis of novel subtilisin inhibitors in
which a human standard mechanism inhibitor, such as pancreatic
secretory trypsin inhibitor, has at least one amino acid of the
reactive site substilisin is reduced by at least a factor of 100.
The novel subtilisin inhibitors (see AAW26362-64) combine the low
allergenicity of human standard mechanism inhibitors, which are not
specific for subtilisin, and the high affinity of non-human
subtilisin inhibitors such as Streptomyces subtilisin inhibitor and
turkey mucoid third domain problems of allergenicity in detergent
curkey macoid third domain problems of allergenicity in detergent
commulations, and can also be used in affinity purification and
constants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; respiratory antigen; respiratory disorder; throat disorder; lung disorder; nose disorder; lung cancer; gene therapy; cytostatic; anti allergic; anti asthmatic; anti inflammatory; olfactory; respiratory active; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomic sequence #463 encoding for novel human respiratory antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       46.5%; Score 24.2; DB 18; Length 1173; 78.4%; Pred. No. 23;
                                                                                                                     Modified subtilisin inhibitor - having altered reactive site resulting in decreased immunogenicity, used in detergent
                                                Schmidt B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                           Estell DA, Fisher J, Hartman C, McGrath M,
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2000US-0180628.
2000US-0184664.
2000US-0186350.
2000US-0189874.
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Matches 29; Conservative
              (ARRI-) ARRIS PHARM CORP
                                                                         WPI; 1997-259023/23
                                                                                        P-PSDB; AAW26365
                                                                                                                                                     composition(s)
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24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
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2000US-0225214.
2000US-0225266.
2000US-0225267.
2000US-0225268.
2000US-0225270.
2000US-0225447.
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2000US-0225759.
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2000US-0226279.
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2000US-0227182.
2000US-0227009.
2000US-0218290
2000US-0220963
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2000US-0239937.
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Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the respiratory system including respiratory cancers and also for testing and detection {\rm e.g.} diagnosis -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ruben SM;
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2000US-0246613.
2000US-0249207.
2000US-0249208.
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2000US-0249265.
2000US-0249297.
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                                                             2000US-0241826.
2000US-0244617.
2000US-0246474.
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2000US-0246609.
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2000US-0249213.
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2000US-0256719.
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01-DEC-2000;
05-DEC-2000;
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05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
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08-NOV-2000;
08-NOV-2000;
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08-NOV-2000;
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17-NOV-2000;
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08-NOV-2000;
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                                   20-OCT-2000;
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                                                                        01-NOV-2000
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                                                                                                                           human respiratory antigens.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to novel genes (AAH68727-AAH73383) associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
invention are useful for preventing, treating and/or prognosing disorders related to the respiratory system including throat disorders (e.g. vocal cord paralysis, tonsillitis, and laryngitis), lung disorders e.g. pneumonia, allergic disorders e.g. asthma, pleurisy, cystic fibrosis, emphysema, nose disorders and cancers of the respiratory tissues e.g. lung cancer. The polynucleotide sequences of the invention are useful in gene therapy and antisense therapy. AAS28161-AAS28764 represent genomic sequences encoding for novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid for diagnosing and treating cervical cancer and for assessing and detecting compounds for treating the cancer \,^{-}
                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                      Length 15366;
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                                                                                                                                                                                                          Seguence 15366 BP; 4516 A; 2790 C; 3055 G; 5005 T; 0 other;
                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                   Db 15172 ACAGAATTTTCAATGTAAATTAAAACGAAGCTGTTACCTTGCTGG 15128
                                                                                                                                                                                                                                                                                                                   2 ataaaagattccatttggataagaacgaatctgttactttgcttg 46
                                                                                                                                                                                                                                                                                       13;
                                                                                                                                                                                                                                                         DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cervical cancer marker nucleic acid 1766
                                                                                                                                                                            at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                        Pred. No. 36;
                                                                                                                                                                                                                                                    Query Match

Best Local Similarity 71.1%; Pred. No. 36
Matches 32; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                               AAH70492 standard; cDNA; 575 BP
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2000US-0203791.
2000US-0210600.
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99US-0171350.
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12-MAY-2000;
09-JUN-2000;
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21-DEC-1999;
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cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-mallygnant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to select and/or assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be

Sequence 575 BP; 190 A; 85 C; 119 G; 181 T; 0 other;

gene therapy.

useful

Human immune/haematopoietic antigen genomic sequence SEQ ID NO:41577.

(first entry)

07-NOV-2001

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                                                                                                                                                                                                                                                                                     Cervical cancer; cytostatic; pre-malignant condition; gene therapy; ss.
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                                  Gaps
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   DB 22; Length 575;
                               Indels
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                                                                                                                                                                                                                                                       Human cervical cancer marker nucleic acid 4454.
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Score 23.4; DB; Pred. No. 39; 0; Mismatches
                                                                        392 TCCTTTTTGGATAAAAACGTATCTGTTGCTTTG 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           774 TCCTTTTGGATAAAAACGTATCTGTTGCTTTG 742
                                                       10 ttccatttggataagaacgaatctgttactttg 42
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                                                                                                                                                             AAH73180 standard; cDNA; 1113
45.0%;
81.8%;
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2000US-0189315.
2000US-0203791.
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12-WAY-2000; 20000S-0203791.
09-JUN-2000; 20000S-0210600.
21-JUL-2000; 2000US-0220114.
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                                                                                                                                                                                                                            (first entry)
                             Conservative
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Query Match
Best Local Similarity
Matches 27; Conserv
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ID AAK867
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Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                      cytostatic; gene therapy; vaccine; metastasis; ds.
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2000US-0224518.
2000US-0224519.
2000US-0225213.
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2000US-0226868,
2000US-0227182,
2000US-0227009,
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2000US-0225266.
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2000US-0225447.
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2000US-0215135.
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2000US-0218290.
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2000US-0225268.
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2000US-0225758.
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2000US-0226279.
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2000US-0189874
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2000US-0230437.
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28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
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22-Aug-2000;
22-Aug-2000;
22-Aug-2000;
33-Aug-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
                                                                                       Homo sapiens.
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11-JUL-2000;
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14-AUG-2000;
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14-AUG-2000;
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14-SEP-2000;
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2000US-0251479

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2000US-0249211.
2000US-0249212.
2000US-0249213.
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2000US-0249215.
2000US-0249216.
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2000US-0239935.
2000US-0239937.
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2000US-0249218.
2000US-0249244.
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                         2000US-0233065
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                                                                          29-SEP-2000;
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02-OCT-2000;
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)

contains and polynucleotides may be used in the prevention, diagnosis and

creample, they may be used to treat disorders associated with decreased

creample, they may be used to treat disorders associated with decreased

creample, they may be used to treat disorders associated with decreased

creample, they may be used to treat disorders in a patient's genome

creamplement the patients own production of (I). Additionally, (I)

supplement the patients own production of (I). Additionally, (I)

polynucleotides may be used to produce the secreted (I), by inserting

the nucleic acids into a host cell and culturing the cell to express the

protein. (I) proteins and polynucleotides may be used to prevent,

diagnose and treat immune/haematopoletic-related diseases, especially

canners and cancer metastases of haematopoletic antigen genomic

to AAK87694 represent human immune/haematopoletic antigen genomic

sequences from the present invention. AAK54912 to AAK84560 and AAM82169
                                                                                                                                                                                                                                                                               Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -
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                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 41577; 3071pp + Sequence Listing; English.
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Best Local Similarity 67.3%; Pred. No. 75;
Matches 33; Conservative 0; Mismatches 16; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Db 19017 AACAATAAATTCCATTTAGTTAAGAAATTTTCAGTTCTGGGTCTTGCAG 18969
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                                               08-DEC-2000; 20000S-0251869.

08-DEC-2000; 20000S-0251989.

08-DEC-2000; 20000S-0251990.

11-DEC-2000; 20000S-0254097.

05-JAN-2001; 2001US-0259678.
                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
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             2000US-0251856.
2000US-0251868.
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             08-DEC-2000;
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08-DEC-2000;
08-DEC-2000;
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31-JAN-2000; 2000US-0179065

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04-FEB-2000; 2000US-0180628.
24-FEB-2000; 2000US-0180628.
16-NAR-2000; 2000US-0180530.
16-NAR-2000; 2000US-01801350.
17-NAR-2000; 2000US-019076.
18 APR-2000; 2000US-0190076.
18 APR-2000; 2000US-0190076.
19 -NAY-2000; 2000US-0190076.
28 JUN-2000; 2000US-0200467.
29 JUN-2000; 2000US-0217496.
11-JUL-2000; 2000US-0217496.
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11-JUL-2000; 2000US-0217496.
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14-AUG-2000; 2000US-022566.
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14-SEP-2000; 2000US-023299.
14-SEP-2000;
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02-OCT-2000; 2000US-0237038.
02-OCT-2000; 2000US-0237040.
13-OCT-2000; 2000US-023935.
13-OCT-2000; 2000US-023937.
20-OCT-2000; 2000US-023937.
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20-OCT-2000; 2000US-0249218.
20-OCT-2000; 2000US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Rosen CA, Barash SC, Ruben SM

WPI; 2001-483426/52.

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CDS
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AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM8110 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein (I) proteins and polynucleotides may be used to produce the secreted (I), by inserting diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/manatopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54595 and AAM82169 represent invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "previously identified as MORF-20078, the encoded protein shows 35.43 percentage identity to the Bacillus subtilis hypothetical protein covered in accession number
                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Previously identified as MORF-20076, the encoded protein shows 27.59 percentage identity to thymidylate kinase (CDC8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 megabase shotgun sequencing method; open reading frame; ORF; ss.
 Disclosure; SEQ ID NO 41578; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                 Length 25806;
                                                                                                                                                                                                                                                                                        .,
                                                                                                                                                                                                                                                                                                                          DD 19020 AACAATAAATTCCATTTAGTTAAGAAATTTTCAGTTCTGGGTCTTGCAG 18972
                                                                                                                                                                                                                                 Sequence 25806 BP; 6061 A; 6546 C; 6450 G; 6749 T; 0 other;
                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       genitalium; DNAA; DNA gyrase; origin of replication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from Saccharomyces cerevisiae"
                                                                                                                                                                                                                                                                 45.0%; Score 23.4; DB 22; ilarity 67.3%; Pred. No. 77; Conservative 0; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GB:D26185_102"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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/label= MG006
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/label= MG010
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/label= MG012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycoplasma genitalium genome.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycoplasma genitalium.
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Best Local Similarity
Matches 33; Conserv
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/note= "Previously identified as MORF-19823, MORF-20080 and MORF-20081, the encoded protein shows 33.04 percentage identity to 5,10-methylene-tetra-hydrofolate dehydrogenase (folD) from E. coli"
                                                                      modification protein (rimK) from Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "previously identified as MORF-19831 and MORF-20106, the encoded protein shows 43.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Previously identified as MORF-19826 and
MORF-20093, the encoded protein shows 46.84
percentage identity to GTP-binding protein
from E. coll"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "previously identified as MORF-20092, the encoded protein shows 45.96 percentage identity to fructose-bisphosphate aldolase (isr) from B. subtilis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "previously identified as MORF-20099, the encoded protein shows 26.82 percentage identity to ATP-dependent nuclease (addA) from B. subtilis"
                                                                                                                                                                                                                                                                                                                                           /note= "Previously identified as WORF-20084, the encoded protein shows 32.23 percentage identity to transport ATP-binding protein (msbA) from E. coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Previously identified as MORF-20100, the encoded protein shows 35.90 percentage identity to glycerol uptake facilitator (glpF) from B. subtilis" complement (39873..40514)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Previously identified as MORF-20101, the encoded protein shows 48.13 percentage identity to thymidylate kinase (tdk) from B. subtilis"
/note= "Previously identified as MORF-20080, the encoded protein shows 31.50 percentage identity to the ribosomal protein S6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Previously identified as MORF-20105, the encoded protein shows 46.83 percentage identity to glycerol kinase (glpK) from E. coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (46268..47422)
                                                                                                                 complement (14396..15217)
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/label= MG035
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/label= MG039
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/label= MG033
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/label= MG038
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/note= "Previously identified as MORF-19834,
MORF-20114 and MORF-20115, the encoded protein
shows 43.02 percentage identity to signal
recognition particle protein (ffh) from B.
subtilis"
                                                                                                                                                                                                                                                                                                                                                            /note= "Previously identified as MORF-2011, the encoded protein shows 29.45 percentage identity to spermidine/putrescine transport system permease protein C (potC) from E. coli"
                                                                                                                                                        "Previously identified as MORF-19832 and MORF-20108, the encoded protein shows 41.92 percentage identity to spermidine/putrescine transport ATP-binding protein (potA) from E. coli.
                                                                                                                                                                                                                                                                  /note= "Previously identified as MORF-20110, the encoded protein shows 26.51 percentage identity to spermidine/putrescine transport
                                                                                                                                                                                                                                                                                                          system permease protein (potB) from E. coli"
 percentage identity to glycerol-3-phosphate dehydrogenase (GUT2) from S. cerevisiae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Previously identified as MORF-20114 and MORF-20115, the encoded protein shows 44.78 percentage identity to purine-nucleoside phosphorylase (deoD) from E. coli"
                                                              "The encoded protein shows 48.86 percentage identity to phosphohistidinoprotein-hexose phosphotransferase (ptsH) from Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Previously identified as MORF-20117, the encoded protein shows 83.03 percentage identity to deoxyribose-phosphate aldolase (deoC) from Mycoplasma pneumoniae"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Previously identified as MORF-20112, the encoded protein shows 36.60 percentage identity to sialoglycoprotease (gcp) from Pasteurella haemolytica"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Previously identified as MORF-20123, the encoded protein shows 38.90 percentage identity to the protein disclosed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Previously identified as MORF-2012,
encoded protein shows 30.25 percent
identity to the protein disclosed in
GB:D26185_99 from B. subtilis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (56970..58310)
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                                                                                                     capricolum" 50060..51520
                                                   /label= MG041
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Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                    Gaps
                                                     /note= "Previously identified as MORF-19845, the encoded protein shows 28.84 percentage identity to glutamic acid specific protease (SPase) from Staphylococcus aureus"
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                                                                                                                                                            "Previously identified as MORF-20136, the encoded protein shows 34.8 percentage identity to ribosomal protein S2 (rpS2)
                                                                                                                                                                                                                                    Score 23.4; DB 18; Length 580073;
Pred. No. 1.38+02;
0; Mismatches 16; Indels 0; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Yamamoto
                                                                                                                                                                                                                                                                                                               Db 438256 aaaatacaccatttgtattgctagcaatatttttttttgatttccgtgc 438304
                                                                                                                                                                                                                                                                                                Otsuki T;
GB:D26185_104 from B. subtilis"
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                                                                                                                                                                                                          from Spirulina plantensis'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 8; SEQ ID 12702; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayashi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cDNA sequence SEQ ID NO:12702.
                                                                                                                                                                                                                                                                                                                                                                                                      AAH14861 standard; cDNA; 2756 BP
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/label= MG067
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                                                                                                                91065..91919
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67.3%;
            81047..82597
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2000JP-0118776.
2000JP-0183767.
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                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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11-JAN-2000;
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                                                                                                                                                                                                                                                                                                                                                                         RESULT 15
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sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence 1s selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length AAH13613 to AAH13612 represent human cDNA sequences; AAB92446 to AAH13631 represent human anno acid sequences; and AAH13629 to AAH13632 represent oligonucleotides, all of which are used in the exemplification of the complification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2756 BP; 911 A; 438 C; 542 G; 865 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                             of the present invention.
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Search completed: June 19, 2002, 17:15:17 Job time: 18975 sec

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Gaps

0;

Query Match

44.6%; Score 23.2; DB 22; Length 2756;
Best Local Similarity 77.8%; Pred. No. 61;
Matches 28; Conservative 0; Mismatches 8; Indels 0;

11 tecatttggataagaacgaatetgttaetttgettg 46

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Sequence 1, Appli
Sequence 6, Appli
Sequence 2, Appli
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3, Appli
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51.668 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-268-992-7
US-09-190-965-2
US-09-303-069-17
US-09-328-111-570
US-08-468-557-3
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US-09-385-982-118
US-08-596-291-1
US-09-100-804-1
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US-09-290-640-45
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Maximum Match 100%
Listing first 45 summaries
                                                                                     - nucleic search, using sw model
                                                                                                                           June 19, 2002, 16:32:51
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OTHER INFORMATION: construct
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PONSTEIN, Anne Silene
RROON-SWART, Saskia
VAN DEVENTETTROOST, Johanna Petronella Els
OHL, Stephan Andres
BRES-VLOEMANS, Alexandra Aleida
                                                                                                                                                                                                                                                                             US-09-462-975-1
Sequence 1, Application US/09462975
Patent No. 6303345
GENERAL INFORMATION:
APPLICANT: Rohde, Wolfgang
APPLICANT: Randles, John W.
APPLICANT: Hehn, Alain
APPLICANT: Salamini, Francesco
TITLE OF INVENTION: USE OF VIRUS DNA AS A PROMOTER
FILE REFERENCE: 23232.0003011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 52; DB 4; I
100.0%; Pred. No. 1.8e-10;
US-08-851-843A-53
US-08-974-249A-220
US-08-854-050-53
US-09-312-312A-1
US-09-500-554-1
US-09-521-526-2
PCT-US95-11859-2
                                                                                        US-09-538-414-7
US-09-091-432-3
US-09-177-249-5
US-09-245-041-3
US-08-846-111D-15
US-08-310-693-1
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US-08-926-724-2
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                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/462,975
CURRENT FILING DATE: 2000-05-17
PRIOR APPLICATION NUMBER: PCT/EP98/04345
PRIOR FILING DATE: 1998-07-13
PRIOR PLICATION NUMBER: 19730502.4
PRIOR FILING DATE: 1997-07-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/08687580B Patent No. 6291647\,
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Matches 52; Conserv
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Sequence

Sequence

5-08-936-165A-33 5-08-920-812-12 5-08-920-827-12 5-08-921-177-12

-08-742-185-101

Sequence Sequence Sequence 1 Sequence 6

US-08-362-577C-12 US-08-920-828-12 US-08-553-619B-6

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LENGTH: 403
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APPLICANT: LOGEMANN, J rgen
APPLICANT: SELA-BUURLAGE, Marianne Beatrix
IIILE OF INVENTION: Antifungal proteins, DNA coding therefor, and
IIILE OF INVENTION: hosts incorporating same
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                              COUNTRY: 100.23

COMPUTER READABLE FORM:
MEDIUM TYPE: 3-1/4" Disk 1.44MB
MEDIUM TYPE: 3-1/4" Disk 1.44MB
COMPUTER: 1BM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: WordPerfect 8 for Windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,580B
FILING DATE: 20-NOV-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/FEP95/00488
FILING DATE: 2-5EP-194
FILING DATE: 2-5EP-194
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 30,086
FILING DATE: 9-7EB-1994
ATTORNEY/AGENT INFORMATION:
NAME: MASS. Clifford J.
FELEPROMONICATION NUMBER: 30,086
FELERBANCE/DOCKET NUMBER: 30,086
FELERBANCE/DOCKET NUMBER: 30,086
FELERBANCE/DOCKET NUMBER: 0-1010885-8
FELERBANCE/DOCKET NUMBER: 0-1010885-8
FELEFAX: (212) 246 8959
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TISSUE TYPE: leaf
INMEDIATE SOURCE:
CLONE: lambda 3
FEATURE:
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ORIGINAL SOURCE:
                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: LADAS & PARRY
STREET: 26 WEST 61 STREET
CITY: NEW YORK
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: ROBISON, KEITH E.

APPLICANT: ROBISON, KEITH E.

TITLE OF INVENTION:

TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES ENCODING HUMAN KINASE AND

TITLE OF INVENTION: PHOSPHATASE HOMOLOGUES AND USES THEREFOR

FILE REPERBNCE: MNI-090

CURRENT APPLICATION NUMBER: US/09/387,212A

CURRENT FILING DATE: 1999-08-31

NUMBER OF SEQ ID NOS: 18

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                        0;
join(774..911, 1045..1154, 3105..3375, 4226..4328, 4432..4777, 4891..5253, 5336..5414, 5531..5743)
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                                                                                                                                                                                                                                                                                                         DB 4; Length 6305;
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44.2%; Score 23; DB 4; Length 403;
Best Local Similarity 66.7%; Pred. No. 5.5;
Matches 32; Conservative 0; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 1936 AAAAAAGAGTCTAGTTGGATATAAGCGAGTCTTTCGTTTTCTT 1979
                                                                                                                                                                                                                                                                                                                                                                                                          45
                                                                                                                                                                                                                                                                                                                                                                                                          2 ataaaagattccatttggataagaacgaatctgttactttgctt
                                                                                                                                                                                                                                                                                                      44.6%; Score 23.2; Di
70.5%; Pred. No. 7.6;
tive 0; Mismatches
                                                                                                                                                                                COCATION: 6095..6100
COTHER INFORMATION: /label= putative US-08-687-580B-6
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APPLICANT: GONEZ, LEONEL JORGE
APPLICANT: SARAS, JAN
APPLICANT: CLESSON-WELSH, LENA
APPLICANT: CLESSON-WELSH, LENA
APPLICANT: HELDIN, CARL-HENRIK
TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
TITLE OF INVENTION: TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 4
CORRESPONDENCE: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                        APPLICATION TENDES, WILSON O., ET AL.
TITLE OF INVENTION: NOVEL HUMAN GENE AND GENE EXPRESSION
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS: II
FILE REFERENCE: CCDMA.266XX
CURRENT FILING DATE: 1999-08-30
EARLIER APPLICATION NUMBER: 09/328,111
EARLIER FILING DATE: 1999-06-08
EARLIER FILING DATE: 1999-06-08
EARLIER FILING DATE: 1999-06-08
EARLIER FILING DATE: 1999-06-31
NUMBER: FEDENCHION NUMBER: 60/107,393
EARLIER FILING DATE: 1999-08-31
NUMBER: PESED ID NOS: 544
SOFTWARE: FESESE for Windows Version 3.0
SEQ ID NO 118
LEAGTH: 578
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44.2%; Score 23; DB 4; Length 578;
Best Local Similarity 74.4%; Pred. No. 5.9;
Matches 29; Conservative 0; Mismatches 10; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 atttggataagaacgaatctgttactttgcttgcagtgc 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C. STREET: 600 ATLANTIC AVENUE
STREET: BOSTON
STATE: MASSACHUSETTS
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/115,573
FILING DATE: 01.5EP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/596,291
FILING DATE: 09-AUG-1996
                     Sequence 118, Application US/09385982 Patent No. 6262334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCATION: (1)...(578)
CTHER INFORMATION: n = A,T,C or G
US-09-385-982-118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08596291
Patent No. 5821075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Homo sapiens
                                                                           GENERAL INFORMATION:
-09-385-982-118/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02210
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US-08-596-291-1
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TITLE OF INVENTION: PRIMARY STRUCTURE AND FUNCTIONAL
TITLE OF INVENTION: EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
TYROSINE PHOSPHATASES
NUMBER OF SEQUENCES: 34
CORRESSPONDENCES: 34
ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
43.8%; Score 22.8; DE
Best Local Similarity 71.4%; Pred. No. 11;
Matches 30; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: WOLF, GREENFIELD & SACKS, P.C. 600 ATLANTIC AVENUE
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: L0461/7000
TELECOMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
TELEFAX: 617/720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/09943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/596,291
FILING DATE: 09-AUG-1996
APPLICATION NUMBER: US 08/115,573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: GONEZ, LEONEL JORGE
APPLICANT: SARAS, JAN
APPLICANT: CLAESS, JAN
APPLICANT: HELDIN, CARL-HENRIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-100-804-1; Sequence 1, Application US/09100804; Patent No. 6066472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: GATES, EDWARD R. REGISTRATION NUMBER: 31,616
                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 01-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 8040 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                        TELEFAX: 617/720-2441
TELEX: 92-1742 EZEKIEL
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRALL
STREET: 600 CITY: BOSTON
TIME: MASSACHUSETIS
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78..7475
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ZIP: 02210
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                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION:
US-08-596-291-1
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GENERAL INCORNATION:
APPLICANT: Dean, Nicholas M.
APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Compound Modulation of Fas Mediated Signaling FILE REPERENCE: ISPH-0351
CURRENT APPLICATION NUMBER: US/09/290,640
CURRENT FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
43.8%; Score 22.8; DB 4; Length 8119;
Best Local Similarity 71.4%; Pred. No. 11;
Matches 30; Conservative 0; Mismatches 12; Indels 0;
                                                                                                                                                                                                                                                    DB 5; Length 8043;
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; Patent No. 6346606
; GENBRAL INFORMATION:
ATPLE OF INVENTION: Protein Containing an SRCR Domain; TITLE OF INVENTION: Protein Containing an SRCR Domain; FILE REFERENCE: 4121-108
; CURRENT APPLICATION NUMBER: US/09/341,587
; CURRENT FILING DATE: 1999-08-31
; EARLIER APPLICATION NUMBER: PCT/DE98/00096
                                                                                                                                                                                                                                                                                                                                             6 aagattocatttggataagaacgaatctgttactttgcttgc 47
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                                                                                                                                                                                                                                                                       Pred. No. 11;
                                                                                                                                                                                                                                                      43.8%; Score 22.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DATABASE ACCESSION NUMBER: D21209/Genbank;
DATABASE ENTRY DATE: 1999-02-05
US-09-290-640-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 45, Application US/09290640
; Patent No. 6204055
                                        CDNA to mRNA
                                                                                                                                                                                                                                                                         71.48;
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 71.44
Matches 30; Conservative
                                                                          ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: HOMO SAPIENS
  single
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PUBLICATION INFORMATION:
JOURNAL: FEBS Lett.
                                                                                                                                                       CDS
78..7478
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                      linear
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STRANDEDNESS:
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                      TOPOLOGY: lin
MOLECULE TYPE:
HYPOTHETICAL: 1
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200-206
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                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
US-09-290-640-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 8119
                                                                                                                                                         NAME/KEY:
                                                                                                                                                                         ; LOCATION:
PCT-US94-09943-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                     FEATURE
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EXPRESSION OF NUCLEOTIDE SEQUENCES FOR NOVEL PROTEIN
TYROSINE PHOSPHATASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 43.8%; Score 22.8; DB Best Local Similarity 71.4%; Pred. No. 11; Matches 30; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LO461/7000WO
    LO461/7003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 01-SEP-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/115,573
FILING DATE: 01-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPTR: USA
COMPUTR: READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTRE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application PC/TUS9409943
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: P 38,349
REFERENCE/DOCKET NUMBER: LO461
TELECOMMUNICATION: INFORMATION:
TELEPHONE: 617/720-3500
TELEFAX: 617/720-3441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
STREET: 600 ATLANTIC AVENUE
                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 92-1742 EZEKIEL INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                    MOLECULE TYPE: CDNA to mRNA
                                                                                                   INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 8043 base pairs
TYPE: nucleic acid
    REFERENCE/DOCKET NUMBER:
                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 8040 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TWOMEY, MICHAEL J
                                                                                                                                                                                                                                                                                                 ORGANISM: HOMO SAPIENS
                                                        TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MASSACHUSETTS: USA
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78..7475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                          ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                      HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY:
; LOCATION:
US-09-100-804-1
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                       Db 23544 AAGATCCCACTCTACAAAAAATTTGTTAATTAGCTGGGTGTG 23499
                                                                                                                                                                                                                                                                                               6 aagattecatttggataagaaegaatetgttaetttgettgeagtg 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARES PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,067
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/213,361
FILING DATE: 14-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/607,293
FILING DATE: 30-OCT-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T-Cadherin Adhesion Molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08474067
Patent No. 5811518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
EARLIER FILING DATE: 1998-01-09
NUMBER OF SEQ 1D NOS: 12
SOFTWARE: Patentin Ver. 2.1
SEQ 1D NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ranscht, Barbara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3959 base pairs
                                                                                                                                                                                                             Query Match 42.35
Best Local Similarity 67.45
Matches 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     United States
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Best Local Similarity 68.29
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: T-C
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-341-587-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45..2181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U
                                                                                    LENGTH: 28720
                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-474-067-1/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LOCATION:
US-08-474-067-1
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3318 GAATACACTTAGATAATAGGCATCTGTTTCCTCCTTGCACTG 3275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,068A
                                                             GENERAL INFORMATION:
APPLICANT: Ranscht, Barbara
TTTLE OF INVENTION: T-Cadherin Adhesion Molecule
NUMBER OF SEQUENCES: 9
                                                                                                                                                                        ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.5%; Score 21.6; DB 2; I 68.2%; Pred. No. 27; tive 0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: T-Cadherin Adhesion Molecule NUMBER OF SEQUENCES: 8 CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: Campbell and Flores STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/474,068A FILING DATE: 07-JUN-1995 CLASSIFICATION: 514 PRIOR APPLICATION 514 APPLICATION NUMBER: US 08/213,361 FILING DATE: 14-MAY-1994 PRIOR APPLICATION NUMBER: US 08/213,361 FILING DATE: 30-OCT-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 1683
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-904
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                    Sequence 1, Application US/08474068A Patent No. 5837525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08472481
Patent No. 5863804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Ranscht, Barbara
                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 3959 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                 United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 68.28
Matches 30; Conservative
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                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
45..2181
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CITY: San Diego
STATE: California
US-08-474-068A-1/C
                                                                                                                                                                                                                                                                                    92122
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LOCATION:
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                                                                                                                                                                                                                                                               COUNTRY:
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Gaps

0;

14; Indels

0; Mismatches Score 21.6; Pred. No. 27

41.5%;

DB 1; Length 3959;

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; NAME/KEY: modified_base
; LOCATTON: all n positions
; OTHER INFORMATION: n=a, c, g, or
US-09-268-992-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FEATURE: -
; OTHER INFORMATION: 3734805
US-09-190-965-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 71.8
Matches 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
                                                                                                                                                            Best Local Similarity
Matches 30; Conserva
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US-08-795-868-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
                                                                                                                                        Query Match
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APPLICANT: Chen, H.
APPLICANT: Ereimer, N.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND TREATING CHROMOSOME-18P RELATED DISORDERS
FILE REFERENCE: 7853-138
CURRENT APPLICATION NUMBER: US/09/268,992
CURRENT FILING DATE: 1999-03-16
EARLIER FILING DATE: 1999-01-22
EARLIER PILING DATE: 1999-01-22
EARLIER PILING DATE: 1998-10-28
EARLIER PILING DATE: 1998-10-28
EARLIER PILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 60/088,312
EARLIER APPLICATION NUMBER: 60/088,312
EARLIER PILING DATE: 1998-06-05
EARLIER FILING DATE: 1998-06-05
EARLIER FILING DATE: 1998-03-16
NUMBER OF SEQ ID NOS: 84
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DD 3318 GAATACACTIAGATAATAGGGCATCTGTTTTCCTTCTCTTGCACTG 3275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REERRUCE/DOCKET NUMBER: P-LJ 1686
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFRAX: (619) 535-8049
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/213,361
FILING DATE: 14-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/607,293
FILING DATE: 30-0CT-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                         APPLICATION NUMBER: US/08/472,481
FILING DATE: 07-UNN-1995
CLESSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7, Application US/09268992
Patent No. 6342351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41.5%;
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Best Local Similarity 68.23
Matches 30; Conservative
                                        United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: single
                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
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San Diego
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
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LENGTH: 72604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
                                        COUNTRY:
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US-09-268-992-7
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GENERAL INFORMATION:
APPLICANT: Lee, Mu-En
APPLICANT: High, Chung-Ming
APPLICANT: High, Chung-Ming
APPLICANT: HIGH, Chung-Ming
ATTLE OF INVENTION: A SINGLE GENE ENCODING AORTIC-SPECIFIC
TITLE OF INVENTION: AND STRIATED-SPECIFIC MUSCLE CELL ISOFORMS AND USES THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
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DB 4; Length 72604;
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                                                                                        41.5%; Score 21.6; DB 4; ... illarity 68.2%; Pred. No. 45; Conservative 0; Mismatches 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,868
                                                                                                                                                                                                                                                                                                                  APPLICANT: Tang, Y Tom
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Gorley, Neil C.
APPLICANT: Gorgone, Gina A.
TITLE OF INVENTION: CALCIUM BINDING PROTEIN
FILE REPRENCE: PF-0635 US
CURRENT PELING DATE: 1998-11-13
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PERL PROGRAM
SOFTWARE: PERL PROGRAM
LENGTH: 1344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17, Application US/08795868 Patent No. 5846773
                                                                                                                                                                                                                                                ; Sequence 2, Application US/09190965
; Patent No. 6071721
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

June 19, 2002, 14:04:31; Search time 7489.97 Seconds (without alignments) 93.704 Million cell updates/sec Run on:

US-09-462-955B-1\_COPY\_734\_785 52 1 aataaaagattccatttgga......tgttactttgcttgcagtgc 52 Title: Perfect score:

Sequence:

IDENTITY\_NUC Gapor 10.0 Gapor 1.0 Scoring table:

13736207 seqs, 6748477542 residues Searched:

27472414 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

EST:\* Database :

em\_gss\_hum: \*
em\_gss\_inv: \*
em\_gss\_pln: \* em\_gss\_vrt:\* em\_estba:\*
em\_esthum:\*
em\_estin:\*
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gb\_esti:\*
gb\_esti:\*
gb\_esti:\* dp\_gss:\* 5: 6: 7: 10: 11: 11: 11: 11: 11: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	AQ106136 HS_3055_A BG749262 602708092	A1065614 ag90e12.x B43802 HS-1058-A2-		BE678889 df57a09.x BE678999 df78a09.x AQ270104 HS_2060_A BE678820 df56a09.x BE678347 df8fa09.x	Æ
SUMMARIES	AQ106136 BG749262 AS547272	AI065614 B43802		BE678889 BE678999 AQ2781004 BE678247	AQ020281 AU122315 CNS049BD
DB	122	1625	1007	10700	12 9 12
Lengt	257 257 999 864	4 18 4 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7	525 576 781	433 485 487 501 560	625 811 904
å Query Match Length DB	50.8	49.6	4 4 4 4 2 8 8 8 6 5 8 8 8 6	4 4 8 9 . 1 4 8 8 . 1 1 . 8 9 4 1	48.1 48.1 48.1
Score	26.4 26.2 26.2	25.8	255.2 255.4 255.4 25.4	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	25 25 25
Result No.	c 2	ი 4 დ გ	ο - - - - - - - - - - - - - - - - - - -	c 11 13 13 14	c 15 16 17

AG506286 RPCT-11-3 AG100388 Pan trog1 BH189468 CO400F04- AG089691 Pan trog1 AA221297 mw08b01.r BF547464 U1-R-C2P- BF674764 U1-R-C2P- BF67464 U1-R-C2P- BF67454 ux59404.y AL021393 ux18a11.y AZ010087 RPCI-23-3 BB67434 AV34444 AX34444 AV34444 BI157582 60292254 AX367139 Tetracodon BF7747468 RC4-BT033 AA228092 Zr55412.s AW037099 614055404 AQ135393 HS_3049_B BF728680 1000065F0 AW83431 AW83431 BM382402 MEST549-B BM380465 MEST52-G BG842500 MEST52-G BG842500 MEST31-FC	BF630600 HVSMEb001 AL077765 Drosophi1 BF062027 7K70f04.x
ब ब ब ब ब ब ब ब	BF630600 CNS00KH0 BF062027
5577 12 6648 12 713 12 713 12 713 12 713 12 713 12 713 12 713 12 713 12 714 71 715 12 715	711 10 101 12 312 10
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44444444444444444444444444444444444444	46.5 46.5 46.2
44444444444444444444444444444444444444	24.2 24.2 24
11122222222222222222222222222222222222	
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## ALIGNMENTS

AQ106136  4.205_A2_B07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone plate=3055 Col=14 Row=C, DNA sequence. AQ106136  GSS. human Homo sarions	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 257) Mahalias, G.C., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and	Acquerce-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589 Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington	401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3887 Email: jwallace@u.washington.edu Sequence Tagged Connector Sequence Tagged Connector Location/Qualifiers Li.257 /Organism="Homo sapiens" /db_xref="taxon:9606" /clone="plate=3055 Col=14 Row=C"
RESULT 1 AQ106136 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS	TITLE JOURNAL MEDLINE COMMENT	FEATURES

ORIGIN

RESULT

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SOURCE

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High quality sequence start: 16
High quality sequence stop: 811.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="HM1:IMSS"
                                                                                                                                                                                                                                                                                                                                                                                          Seq primer: M13-Reverse
                                 AZ547272.1 GI:11169813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AI065614.1 GI:3341021
genomic, DNA sequence.
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70.0%;
                                                                        Entamoeba histolytica.
                                                                                        Entamoeba histolytica
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Best Local Similarity 70.0°
Matches 35; Conservative
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Zea mays
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/db_xref="taxon:9666"
/clone=Inb="NHiMGC_43"
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/clone_Inb="NHiMGC_43"
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/tab.host="bH108 (phage=resistant)"
/note="Corgan: eye; Vector: pOTB7; Site_1: XhOI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhOI sites using the following 5'
adaptor: GGCACGAGGG. Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
california, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"
13 a 267 c 311 g 208 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCUS A2547272 864 bp DNA linear GSS 14-NOV-2000 DEFINITION ENTDZ20TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI682 row: h column: 24
High quality sequence stop: 810.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH`MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Pred. No. 43;
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Pred. No. 58;
     91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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     43
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75.0%;
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Best Local Similarity 79.55
Matches 31; Conservative
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     30
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BG749262
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                                                                              Query Match
Best Local Similarity
Matches 33; Conserv
     93 a
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RESULT

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/db_xref="Haxon:5759"
/db_xref="Haxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/clone_lib="Detamoeba histolytica Sheared DNA"
/clone_lib="Wedtor: pH0S1; Site_l: BST i; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution of "2 kBo." The v + i method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
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1 (bases 1 to 418)
Schutz,K., de la Bastide,M., Gnoj,L., Habermann,K., Huang,E.N., Parnell,L.D., Dedhia,N., Martienssen,R. and McCombie,W.R.
                                                                                                                                                                                                                                                                                                                                                                                                                              Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
                                                                  Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HM1:LMSS sheared DNA library
Unpublished (2000)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
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                                                                                                                                                                                                                                                                          The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0208 Fax: 301 838 3543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Entamoeba histolytica"
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Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 864)
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0;

Gaps

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1 (bases 1 to 537)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GSS 06-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HS_2 = 1000 - A_2 - H06 - T CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2100 Col=12 Row=O, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: (206) 616-3618

Fmax: (206) 616-3887

Fmax: (206) 616-3887

Clones may be purchased from Research Genetics (info@resgen.com).

Plate: 2100 row: 0 column: 12

Seq primer: T7
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                             /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
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/organism="Homo sapiens"
/db_xref="texon:9606"
/clone="Plate=CT 780 Col=12 Row=G"
/clone_lib="CIT Human Genomic Sperm Library C"
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University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
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                                                                                                                                                                                                                                                                                                                    1 aataaaagattccatttggataagaacgaatctgttactttgctt 45
                                                                                                                                                                                                                                Score 25.8; DB 12;
Pred. No. 74;
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/clone="Plate=2100 Col=12 Row=0"
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Best Local Similarity 73.3%;
Matches 33; Conservative
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                                                                               /sex="M"
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Matches 33; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="immature ear"
/note="Vector: pBLUESCRIPT SK+ (X52325); Site_1: XhoI;
Site_2: ECORI; This library is described in Schmidt, Hake,
et al., (1993) Plant Cell 5:729-737. CDNAs are
directionally cloned into the XhoI and EcoRI sites; XhoI
snear the polyA tall. Most reads from this library are
3' in direction. Additional information on this library as
well as ftp access to all sequences can be found at
http://www.cshl.org/maizegnome"
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1 (bases 1 to 487)
Mahairas, G.G., Zackrone, K.D., Smith, T., Tipton, S., Schmidt, S., Tralooff, R., Abajlan, C., Blanchard, A., West, A. and Bood, L.E. Construction of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analysis of 20,000 Sequence
                                                                                                                                                                                                                                                                                                                                                            /clone="ag90e12"
/clone_lib="maize inflorescence immature ear library"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HS-1058-A2-D06-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 780 Col=12 Row=G, DNA sequence.
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0
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Pred. No. 73;
0; Mismatches 12; Indels (
                                                                           Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mccombie@cshl.org
Plate: a990 row: e column: 12
Seq primer: M13 forward universal -21
High quality sequence stop: 18.
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                                                                Lita Annenberg Hazen Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1997)
Contact: Mahairsa GG, Zackrone KD, Hood L
University of Washington
Seattle, WA 98195, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
Expressed sequence tags from Z. mays Unpublished (1998)
Contact: W. Richard McCombie
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Sequence Tagged Connector
Plate: CT 780 row: G column: 12
Class: BAC ends
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                                                                                                                                                                                                                                                                                            /organism="Zea mays"
/cultivar="B73"
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(206) 685-7301
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Best Local Similarity 73.3*
Matches 33; Conservative
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Gaps

484 ATAAAACACCCGAATTGCATAATAAAGACCCTATGACTTTGTGTACAGTAC 434

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases I to 525)
Dunn, D., Aoyaqi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly and Wright, D., Weiss, R., Stokes, R., Tingey, A., von Niederhausern, A. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                      AZ390369 525 bp DNA linear GSS 03-OCT-200 IM0151M10R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCLM0151M10 R, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plate: 0151 row: M column: 10
Seq primer: CACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0151M10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         High quality sequence stop: 525.
Location/Qualiflers
1. .525
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Plate: 0151 row: M
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Fax: 801 585 7177
                                                                                                                                                                                                                                         house mouse.
                                                                                                                                                                                                                                                                        Mus musculus
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RESULT 7
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 576)

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, T., Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Glabbons, M., McCann, R., Cole, R., Tsagareishvill, R., Williams, T., Endocrine Pancreas Consortium
Onpublished (2000)
Other ESTS: 1539d66,x1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Organ: Parcreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; CDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size -1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-36-1916, Fax: 314-747-2692."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     601505608F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3907441 5', BE884333
                                         EST 05-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Endocrine Pańcreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: dmeltonébiohp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
(hinoue@im.wustl.edu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
                               1539406.yl HR85 islet Homo sapiens CDNA 5', mRNA sequence.
BG654372
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/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
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Pred. No. 1e+02;
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/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (hinoue@im.wustl.edu)
Seq primer: -40RP from Gibco
High quality sequence stop: Location/Qualifiers
                                                                                                                   BG654372.1 GI:13791781
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 617-495-1812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 617-495-8557
                                                                                                                                                                                          Homo sapiens
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Best Local Similarity
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Query Match . 48.8%; Score 25.4; DB 12; Best Local Similarity 68.6%; Pred. No. 1e+02; Matches 35; Conservative 0; Mismatches 16;

Length 525;

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Xenopodinae; Xenopus.
1 (bases 1 to 456)
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.
Amartin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person
Waterston,R., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             df78a09.x1 Xenopus laevis occyte non normalized Xenopus laevis cDNA clone IMAGE:3745432 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from 2ug of poly A+ RNA.
BCORT-XhoI cut cDNA was then ligated into Unizapa. K
(Stratagene) with EcoRI at the 5' end and XhoI at the 3'
end. SS-library phagemids were prepared by mass excision
from the original library and normalized by hybridization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST 18-APR-2001
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Library normalized by Jihwan Song
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clone distribution information for
this library can be found through Research Genetics, visit their
web page at: http://www.resgen.com/ Please reference the id listed
below when ordering this clone: Source lab clone id - xlnneg002ml7
Seq primer: -40UP from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   electroporated into Top-10 F'. Original library contruction by Bruce Blumberg (Blumberg et al., 1991 Science 253, 194-196; Hawlet et al., 1995, Genes Dev. 9, 2923-2935). Note: This is a Xenopus Gene Collection (XGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Xenopus laevis unfertilized egg cDNA library"
/tissue_type="unfertilized egg"
/lab_host="Top-10 F'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washu Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
TT = 314 286 1810
Fax: 314 286 1810
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1 Similarity 69.4%; Pred. No. 1.4e+02;
34; Conservative 0; Mismatches 15
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Library normalized by Jihwan Song
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                                                                                                                                                                                                                                                                                                                                                           /organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="IMAGE:3743416"
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Unpublished (1999)
                                                                                                                                                                                                                                                             High quality sequence stop: 423.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 g
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                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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116 c
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1 (bases 1 to 433)
1 (bases 1 to 433)
1 (bases 1 to 434)
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1 (bases 1 to 437)
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2 (bases 1 to 437)
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3 (bases 1 to 47)
4 (bases 1 to 47)
4 (bases 1 to 47)
5 (bases 1 to 47)
6 (bases 1 to 43)
6 (bases 1 to 43)
6 (bases 1 to 47)
6 (bases 1 to
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/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT
A versage insert size 2.1 kb. 1 others
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Marican clawed frog.

Evenopus laevis

Evenopus hetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Metazoa; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                    Homo sapiens
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 781)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM9717 row: p column: 02
                                                                                                                                                                                                                                                                                  NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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Fax: 314 286 1810
Enail: est@watson.wustl.edu
Library constructed by Bruce Blumberg
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Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
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Unpublished (1999)
Contact: Sandy Clifton, Ph.D.
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tissue Procurement: ATCC
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Gaps

High quality sequence stop: 487.

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/clone="IMAGE:37452"
/clone=lib="Xenopus laevis oocyte non normalized"
/tissue_type="aocyte (stages 5 and 6)"
/lab host="Top-10 F'"
/note="Vector: PBluescript SK-; Site_1: ECORI; Site_2:
Xhoi; CDNA was prepared from 2ug of poly A+ RNA.
ECORI-Xhoi cut CDNA was then ligated into Unizap.xR
(Stratagene) with ECORI at the 5' end and Xhoi at the 8'
end. SS-library phagemids were prepared by mass excision from the original library and normalized by hybridization to biotinylated driver (prepared from the same library by PCR) to Cot-omega of 11. After removal of hybrids and excess driver by streptavidin sephanose chromatography,
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Xenopus clone distribution information for this library can be found through Research Genetics, visit their web page at: http://www.resgen.com/ Please reference the id listed below when ordering this clone: Source lab clone id - xlnnoc002a17 High quality sequence stop: 453.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the ss-phagemids were made double stranded and electroporated into Top-10 F'. Original library contruction by Bruce Blumberg (Blumberg et al., 1991 Science 253, 194-196; Hawlet et al., 1995, Genes Dev. 9, 2923-2935). Note: This is a Xenopus Gene Collection (XGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HS_2060_A1_E04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2060 Col=7 Row=1, DNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence-tagged connectors: A sequence approach to mapping and
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University of Mashington
Vall Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Indels
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Pred. No. 1.4e+02;
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Best Local Similarity 69.4%;
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122 c
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Class: BAC ends
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Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D., Martin,J., Wylle,T., Underwood,K., Theising,B., Bowers,Y., Person,B., Glbbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R., Washu Ser project, 1999
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 18-APR-2001
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Library normalized by Jihwan Song
Dan Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clone distribution information for
this library can be found through Research Genetics, visit their
web page at: http://www.resgen.com/ Please reference the id listed
below when ordering this clone: Source lab clone id - xlnneg002il7
High quality sequence stop: 494.
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/tissue_type="unfertilized egg"
/tissue_type="unfertilized egg"
/lab_host="rop-10 F"
/note="vector: pBluescript SR-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from 2ug of poly A+ RNA.
EcoRI-XhoI cut cDNA was then ligated into Unizap-XR
(Stratagene) with EcoRI at the 5' end and XhoI at the 3'
end. SS-library phagemids were prepared by mass excision from the original library and normalized by hybridization
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                   /clone="Plate=2060 Col=7 Row=I"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
                                                                                                                                                                                   /note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"
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501 bp mRNA linear EST 18-APR-2 df55a09.x1 Xenopus laevis unfertilized egg cDNA library Xenopus laevis cDNA clone IMAGE:3743320 3', mRNA sequence.
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Fax: 314 286 1800
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1 Similarity 69.4%; Pred. No. 1.4e+02;
34; Conservative 0; Mismatches 15; Indels
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WashU Xenopus EST project, 1999
Washington University School of Medicine
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                                                    /organism="Homo sapiens"
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                                                                                /db_xref="taxon:9606"
  Location/Qualifiers
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PCR) to Cot-omega of 11. After removal of hybrids and

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/clone="IMAGE:3146116"
/clone=lib="Xenopus laevis oocyte non normalized"
/tissue_type="oocyte (stages 5 and 6)"
/lab_host="Top-lo" (stages 5 and 6)"
/lab_host="Top-lo" (F'"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: EcoRI
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1 (bases 1 to 560)
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.
Amtin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person
,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
Waterston,R. and Wilson,R.
WashU Xenopus EST project, 1999
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Library constructed by Bruce Blumberg
Library constructed by Jihwan Song
Library normalized by Jihwan Song
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Xenopus clone distribution information for
this library can be found through Research Genetics, visit their
web page at: http://www.resgen.com/ please reference the id listed
below when ordering this clone: Source lab clone id - xlnnoc003n05
Seq primer: -400p from Gibco
High quality sequence stop: 488.
to biotinylated driver (prepared from the same library by PCR) to Cot-omega of 11. After removal of hybrids and excess driver by streptavidin sepharose chromatography, the ss-phagemids were made double stranded and electroporated into Top-10 F'. Original library confruction by Bruce Blumberg (Blumberg et al., 1991 Science 253, 194196; Hawlet et al., 1995, Genes Dev. 9, 2923-2935). Note: This is a Xenopus Gene Collection (XGC)
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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/db_xref="taxon:8355"
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Contact: Sandy Clifton, Ph.D.
WashU Xenopus EST project, 1999
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AQ020281 625 bp DNA linear GSS 09-JUN-1998 CIT-HSP-2307A3.TF CIT-HSP Homo sapiens genomic clone 2307A3, DNA
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 622)
Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Goldden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
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             the ss-phagemids were made double stranded and electroporated into Top-10 F' Original library contruction by Bruce Blumberg (Blumberg et al., 1991 Science 253, 194-196; Hawlet et al., 1995, Genes Dev. 9, 2923-2935). Note: This is a Xenopus Gene Collection (XGC)
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Seq primer: M13-21
excess driver by streptavidin sepharose chromatography,
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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Query Match

48.1%; Score 25; DB 10;
Best Local Similarity 69.4%; Pred. No. 1.4e+02;
Matches 34; Conservative 0; Mismatches 15;
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ilarity 69.4%; Pred. No. 1.4e+02;
Conservative 0; Mismatches 15.
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/db_xref="taxon:9606"
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Other_GSSs: CIT-HSP-2307A3.TR
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Search completed: June 19, 2002, 14:04:35 Job time: 7533 sec

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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 11:59:02; Search time 247.21 Seconds

(without alignments)
21.860 Million cell updates/sec

Title: US-09-462-955B-1_COPY_655_676
Sequence: 1 ctgcccaggccgaaggcctggg 22
Scoring table: LDENTITY_NUC
Gapop 10.0, Gapext 1.0
Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066
Maximum DB seq length: 0000000000
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued\_Patents\_NA:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description		Sequence 1, Appli Sequence 1, Appli Sequence 6, Appli Sequence 3, Appli Sequence 3, Appli
SUMMARIES	US-09-462-975-6 US-09-462-975-1 US-09-232-200-29 US-09-232-201-29 US-09-232-201-28 US-09-232-197-28 US-09-232-197-28 US-09-232-197-64 US-09-232-201-64 US-09-232-201-64 US-09-232-201-64 US-09-232-201-64 US-09-232-201-64 US-09-232-201-64 US-09-232-201-24 US-09-232-201-24 US-09-232-201-24 US-09-232-201-24 US-09-232-201-24 US-09-232-201-24 US-09-232-201-24 US-09-035-648-23 US-09-035-648-23 US-09-035-648-23	US-09-103-840A-1 US-09-103-840A-1 US-08-811-949-40 US-08-257-341-6 US-08-133-804-3 US-08-461-838-3
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Sequence 1, Appli Sequence 1, Appli Sequence 5, Appli Sequence 60, Appl Sequence 3, Appli Sequence 44, Appl Sequence 46, Appl Sequence 52, Appl Sequence 52, Appl Sequence 54, Appl Sequence 64, Appl Sequence 64, Appli Sequence 64, Appli Sequence 64, Appli Sequence 64, Appli Sequence 64, Appli Sequence 64, Appli Sequence 66, Appli Sequence 1, Appli Sequence 1, Appli	OMOTER Sequence:/note=synthetic	Length 23; ; Indels 0; Gaps 0;
US-08-461-386-3 US-08-73-412-1 US-08-427-640-5 US-08-427-640-5 US-08-811-949-60 US-08-811-949-44 US-08-811-949-46 US-08-811-949-58 US-08-811-949-58 US-08-811-949-58 US-08-811-949-58 US-08-811-949-64 US-08-811-949-64 US-08-811-949-64 US-08-811-949-64 US-08-811-949-64 US-08-811-949-64 US-08-811-949-64 US-08-811-949-64	ALIGNMENTS  5  DNA AS A PRC  7462,975  98/04345  02.4  rsion 4.0	#; Score 22; DB 4; I )%; Pred. No. 0.56; 0; 0; Mismatches 0; 19 22 19 22 462975
779 2 942 3 1065 5 1 1066 5 1 1068 8 1 1068 8 2 1068 8 2 1068 8 2 1068 8 2 1068 8 2 11110 0 11170 2 11170 2 11260 3	SULT 1  -09-462-975-6  Sequence 6, Application US/09462975  EARENT TWENRATION:  APPLICANT: Rende, Wolfgang  APPLICANT: Rende, Wolfgang  APPLICANT: Randles, John W.  APPLICANT: Salamin, Francesco  TITLE OF INVENTION: USE OF VIRUS  FULK REPERBENCE: 2323. 000301  CURRENT FILING DATE: 1998-05-17  PRIOR PAPLICATION NUMBER: PCT/EP9  PRIOR PAPLICATION NUMBER: PCT/EP9  PRIOR PAPLICATION NUMBER: DS/09-05-17  PRIOR PLING DATE: 1997-07-16  NUMBER OF SEQ ID NOS: 7  SOFTWARE: FastSEQ for Windows Ver SEQ ID NOS: 7  TYPE: DNA  ORGANISM: Artificial Sequence  FEATURE: NEVERMATION: CONSTRUCT  OTHER INFORMATION: CONSTRUCT	Query Match Best Local Similarity 100.0%; Matches 22; Conservative 0  Oy 1 ctgcccaggccgaaggcctggg 2
7733.66 7733.66 7733.66 7733.66 7733.66 7733.66 7733.66	pplicati 03345 MATION: Rohde, W Rohde, W Radles, Radles, Radles, Radles, Radles, ATION NU DATE: DATE: DATE: DATE: Trificia ATION NU MATION:	Similarity 22; Conser gcccaggccga
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LENGTH: 1938
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100.0%; Score 22; DB 4; Length 1291;
Best Local Similarity 100.0%; Pred. No. 0.56;
Matches 22; Conservative 0; Mismatches 0; Indels 0
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APPLICANT: Stahl, Andreas
APPLICANT: Stahl, Andreas
APPLICANT: Hissch, David J.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Gimeno, Ruth E.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: WHI97-2193MB
CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 60/031,374
EARLIER APPLICATION NUMBER: 60/031,374
EARLIER FILING DATE: 1998-01-15
EARLIER FILING DATE: 1998-01-204
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FILE REFERENCE: 23.23.000301
CURRENT APPLICATION NUMBER: US/09/462,975
CURRENT FILING DATE: 2000-05-17
PRIOR APPLICATION NUMBER: PCT/FP98/04345
PRIOR APPLICATION NUMBER: 1998-07-13
PRIOR APPLICATION NUMBER: 19730502.4
PRIOR FILING DATE: 1997-07-16
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity 90.5
Matches 19; Conservative
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APPLICANT: Lodish, Harvey F.
APPLICANT: Gineno, Ruth E.
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tartaglia, Louis A.
FILE REFERENCE: WH197-21p3MA
CURRENT APPLICATION NUMBER: US/09/232,197A
CURRENT APPLICATION NUMBER: 06/071,374
EARLIER APPLICATION NUMBER: 60/071,374
EARLIER PILING DATE: 1998-01-15
EARLIER PILING DATE: 1998-01-15
EARLIER PILING DATE: 1998-07-20
EARLIER PILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 1164
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; Patent No. 6288213
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| 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111 | 111
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Best Local Similarity 90.5
Matches 19; Conservative
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US-08-785-241-1/c
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                                                                                                                                                                                       APPLICANT: CALTELLY, MILLEL, ANGUER, APPLICANT: CALTELLY, MACHEN, STITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS FILE REFERENCE: WH197-21pJMB CURRENT APPLICATION NUMBER: 05/09/33,200A CURRENT FILING DATE: 1999-01-14 EARLIER APPLICATION NUMBER: 60/071,374 EARLIER FILING DATE: 1998-01-15 EARLIER FILING DATE: 1998-01-15 EARLIER FILING DATE: 1998-07-20 EARLIER APPLICATION NUMBER: 60/10,341 EARLIER FILING DATE: 1998-12-04 NUMBER OF SEQ ID NOS: 105 SOFTWARE: PASSES FOR WINDOWS VERSION 3.0 SEQ ID NOS: 105 SEQ ID NOS: 105 SEQ ID NOS: 104 SEQ ID NOS: 104 SEQ ID NOS: 104 SEQ ID NOS: 105 SEQ ID NOS: 104 SEQ ID NOS: 104 SEQ ID NOS: 104 SEQ ID NOS: 105 SEQ ID NOS: 104 SEQ ID NOS: 104 SEQ ID NOS: 104 SEQ ID NOS: 105 SEQ ID NOS: 104 SEQ ID NOS: 104 SEQ ID NOS: 104 SEQ ID NOS: 105 SEQ ID NOS: 104 SEQ ID NOS: 105 SEQ ID NOS: 104 SEQ ID NOS: 104 SEQ ID NOS: 104 SEQ ID NOS: 105 SE
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APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tarteqlia, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: WHI99-21p3MA
CURRENT PPLINGE WHIS9-21p3MA
CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 66/071,374
EARLIER PPLICATION NUMBER: 66/071,374
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER FILING DATE: 1998-01-15
EARLIER FILING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/093,491
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NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 3.0
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Patent No. 6300096
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                                         APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
APPLICANT: Gimeno, Ruth E.
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Best Local Similarity 90.5
Matches 19; Conservative
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; ORGANISM: Homo sapiens
US-09-232-200-28
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; ORGANISM: Homo sapiens
US-09-232-197-28
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GENERAL INFORMATION:
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GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NATE:
APPLICATION NUMBER: US/08/785,241
FILING DATE: 17-JAN-1997
                                                                   APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Lodish, Harvey F.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: WH197-21p3MC
                                                                                                                                                                                                                                              FILE NEFERANCE: WALSY-ZIPJAN
CURRENT APPLICATION NUMBER: US/09/232,201A
CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 60/091,374
EARLIER FILING DATE: 1998-01-15
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: PASLEGG FOR WINDOWS Version 3.0
SOFTWARE: PASLEGG FOR WINDOWS Version 3.0
ENGTH: 1941
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Sequence 28, Application US/09232201A Patent No. 6348321
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APPLICANT: MCKNight, Steven L.
APPLICANT: Russell, David W.
APPLICANT: Tian, Hui
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TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,6
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STATE: CALIFORNIA
COUNTRY: USA
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US-09-232-201-28
                                                   GENERAL INFORMATION:
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517 TGCCCAGGCAGAAGGCCAGGG 497
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EARLIER FILING DATE: 1998-12-04
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90.58;
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Best Local Similarity 90.5
Matches 19; Conservative
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US-09-232-200-46/c
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US-09-232-201-64/C
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                                                                                                        TYPE: DNA
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                                                                                                                                             80.9%; Score 17.8; DB 1; Length 2816; 90.5%; Pred. No. 30; tive 0; Mismatches 2; Indels 0
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GENERAL INFORMATION:
APPLICANT: Stabl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglia, Louis A.
ITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: WHI97-21p3MB
CURRENT FAPLICATION NUMBER: US/09/232,200A
CURRENT FILING DATE: 1999-01-14
EARLIER APPLICATION NUMBER: 60/091,374
EARLIER FILING DATE: 1998-01-15
BARLIER FILING DATE: 1998-01-15
EARLIER FILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 105
SEQ ID NO 64
SEQ ID NO 64
LENGTH:: SA17
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APPLICANT: Stahl, Andreas

APPLICANT: Hisch, David J.

APPLICANT: Lodish, Harvey F.

APPLICANT: Gimeno, Ruth E.

APPLICANT: Tartaglia, Louis A.

TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS

FILE REFERENCE: WH197-21p3NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.9%; Score 17.8; 90.5%; Pred. No. 30
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                                                                                                                                                                                                                                                                                                                                                     US-09-232-200-64/c; Sequence 64, Application US/09232200A; Patent No. 6288213; GENERAL INFORMATION:
                                                                                                                                                                                                                                                     2784 CTGCCCAGGTAGAAGGCCTGG 2764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       517 TGCCCAGGCAGAAGGCCAGGG 497
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Best Local Similarity 90.55
Matches 19; Conservative
                                                                                                                                             Query Match
Best Local Similarity 90.5<sup>3</sup>
Matches 19; Conservative
      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Mus musculus US-09-232-200-64
                                          ; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-785-241-1
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Sequence No. 6288213

GENERAL INFORMATION:

APPLICANT: Stahl, Andreas

APPLICANT: Hirsch, David J.

APPLICANT: Gineno, Ruth E.

APPLICANT: Gineno, Ruth E.

APPLICANT: Tartaglia, Louis A.

TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS

FILE REFERENCE: WHI97-2193MB

CURRENT APPLICATION NUMBER: US/09/232,200A

CURRENT FILING DATE: 1999-01-14

EARLIER FILING DATE: 1998-01-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INCORMATION:
GENERAL INCORMATION:
APPLICANT: Stall, Andreas
APPLICANT: Hisch, David J.
APPLICANT: Eddish, Harvey F.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartegila, Louis A.
TITLE OF INVENTION: FATY ACID TRANSPORT PROTEINS
FILE REFERENCE: WH197-21p3MC
CURRENT APPLICATION NUMBER: US/09/232,201A
CURRENT FILING DATE: 1999-01-14
EARLIER FILING DATE: 1998-01-15
EARLIER FILING DATE: 1998-07-20
EARLIER APPLICATION NUMBER: 60/093,491
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-07-20
EARLIER FILING DATE: 1998-07-20
SAFTHER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FASTESE FOR WINDOWS VERSION 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 17.8; DB
Pred. No. 30;
0; Mismatches
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NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 64
LENGTH: 3217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 64, Application US/09232201A
; Patent No. 6348321
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Sequence 46, Application US/09232197A
GENERAL INPORMATION:
APPLICANT: Stahl, Andreas
APPLICANT: Glamen, Bavid J.
APPLICANT: Glamen, Ruth E.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REFERENCE: WH197-21p3AA.
CURRENT FILING DATE: 1999-01-14
EARLIER PILING DATE: 1998-01-15
EARLIER PILING DATE: 1998-01-15
EARLIER PILING DATE: 1998-01-15
EARLIER FILING DATE: 1998-01-15
EARLIER FILING DATE: 1998-01-15
EARLIER FILING DATE: 1998-01-04
EARLIER FILING DATE: 1998-01-04
SARING PAPLICATION NUMBER: 60/10,941
EARLIER FILING DATE: 1998-12-04
SOUTWARE: FESTERE OF SEQ ID NOS: 105
SOFTWARE: FASTERE OF Windows Version 3.0
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Patent No. 6148321
GENERAL INFORMATION:
APPLICANT: Stahl, Andreas
APPLICANT: Hirsch, David J.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Gimeno, Ruth E.
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: FATTY ACID TRANSPORT PROTEINS
FILE REPERBNCE: WHI97-21p3MC
CURRENT APPLICATION NUMBER: US/09/232,201A
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90.5%; Pred. No. 30;
Live 0; Mismatches
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EARLIER APPLICATION NUMBER: 60/093,491
EARLIER FILING DATE: 1998-07-20
EARLIER PEDLICATION NUMBER: 60/110,941
EARLIER FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 46
LENGTH: 3694
                                                                                                                                                                                                                                                                                                                                                                                                                       691 TGCCCAGGCAGAAGGCCAGGG 671
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Matches 19; Conservative
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Best Local Similarity 90.55
Matches 19; Conservative
                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-232-200-46
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; ORGANISM: Homo sapiens
US-09-232-197-46
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; CURRENT FILING DATE: 1999-01-14
; EARLIER APPLICATION NUMBER: 60/071,374
; EARLIER PILLING DATE: 1999-01-15
; EARLIER FILING DATE: 1999-01-15
; EARLIER FILING DATE: 1998-07-20
; EARLIER FILING DATE: 1998-07-20
; EARLIER FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 105
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; SCOTWARE: PastSEQ for Windows Version 3.0
; SCOTWARE: FastSEQ for Windows Version 3.0
; SCOTWARE:
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Thu Jun 20 06:56:45 2002

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

June 19, 2002, 11:59:02; Search time 7489.97 Seconds (without alignments) 39.644 Million cell updates/sec Run on:

US-09-462-955B-1\_COPY\_655\_676 22

Title: Perfect score: Sequence:

1 ctgcccaggccgaaggcctggg 22

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

13736207 seqs, 6748477542 residues Searched:

27472414 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

gb\_gss:\* em\_gss\_hum:\* em\_gss\_inv:\* em\_gss\_pln:\* em\_estba:\*
em\_esthum:\*
em\_estin:\*
em\_estov:\*
em\_estpl:\*
em\_estpl:\*
em\_estpl:\*
em\_htc:\*
gb\_est1:\* gb\_est2:\* gb\_htc:\* EST:\* 10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em\_gss\_vrt:\*

	Description	BG327577 602426566	BE860673 III-M-AH1-	BB147701 BB147701		BB239924 BB239924	BH043080 RPCT-24-3	BT101919 602887615	BF119646 60175751	BIO32357 CM3-NNO24	BB813476 BB813476	AW522130 UT-R-B.TOD	AA158436 zo59h11.r	AW553523 1.0228011-		7	B1295549 III-R-DKO-	
SUMMARIES	ID	BG327577	BE860673	BB147701	BB284196	BB239924	BH043080	BI101919	BF119646	BI032357	BB813476	AW522130	AA158436	AW553523	AI406571	BF403937	BI295549	BI004403
	DB	10	10	6	6	6	12	10	10	10	6	6	6	σ	9	10	10	10
	Query Match Length DB	935	176	238	393	555	608	654	959	291	377	405	438	455	512	517	558	176
ж (	Query	88.2	85.5	85.5	85.5	85.5	85.5	85.5	85.5	83.6	83.6	83.6	83.6	83.6	83.6	83.6	83.6	80.9
	Score	19.4	18.8	18.8	18.8	18.8	18.8	18.8	18.8	18.4	18.4	18.4	18.4	18.4	18.4	18.4	18.4	17.8
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AU058457 AU058457 AW877400 MR4-PT005 AW336731 21454 MAR BE38251 601277687 BE771160 RC5-FT007 BF372847 RC5-FT007 BE771169 RC5-FT007 BI342341 370080 MA BI404521 MI-P-CT1-	BIO24756 PWO-MTO20 AW416678 52227 MAR BF087382 QV2-HT054 AI520113 LD40089.5 AW408256 UT-HF-BKO		BF778233 228614 MA AA405771 Zu57c06.r BI401089 MI-P-CP0- AW416681 52238 MAR BF775369 285513 MA BF444355 262209 MA BF4443589 261137 MA
444	A A A	AW838277 BE818489 BE818183 BE014102 BE013607 AW403812 BG609304	BF078233 AA40571 B1401089 AW416681 BF775369 BF444355
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243 295 313 349 370 371 372 375	383 384 390 392 397	400 4 4 4 1 1 8 9 4 4 3 3 3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5	444 4442 4442 4465 471 79
08888000 0088800 0000 0000 0000 0000 0	00000	0.008 0.008 0.008 0.008 0.008 0.008	
17.8 17.8 17.8 17.8 17.8 17.8 17.8 17.8	17.8 17.8 17.8 17.8	17.8 17.8 17.8 17.8 17.8 17.8	17.8 17.8 17.8 17.8 17.8 17.8
118 222 223 224 254 254	27 28 29 30 31	3 3 3 3 3 3 3 5 3 5 3 5 5 5 5 5 5 5 5 5	2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
0 000000	0 0 0 0	0 0000	00 0000

## ALIGNMENTS

RESULT 1 BG32757/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	
REFERENCE AUTHORS TITLE JOURNAL	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 935) NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Onpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Bmail: capabs-remail.nih.gov  Email: capabs-remail.nih.gov  CDNA Library Preparation: Ling Hong/Rubin Laboratory  CDNA Library Preparation: Ling Hong/Rubin Laboratory  CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  DNA Sequencing by: Incyte Genomics, Inc.  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  http://image.llnl.gov  Plate: LiCM1279 row: d column: 17
FEATURES SOURCE	High quality sequence stop: 789.  Location/Qualifiers  1. 935  /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4564192"
	/Lisbue_Lype="Tenal cell adenocationma" /lab_host="DH108 [phage-resistant)" /note="Organ: kidney; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in

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/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
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/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
              1 ctgcccaggccgaaggcctggg 22
                               71 CTGCTCAGGCCGAAGCCCTGGG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /sex="female"
                                                                                                                                                                                                BB147701.1 GI:8802638
                                                                                                                                                                                                                                                                                                   (bases 1 to 238)
                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                     house mouse.
                                                                                                                                                                                  BB147701
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                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                     ORGANISM
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                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                   ACCESSION
                                                                                                 RESULT
BB147701
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                                                                                                                                                                                                                   KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE
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                                                                                                                                                                                                   VERSION
                                                                                                                                                                                                                                     SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA Library Preparation: M.B. Soares Lab Clone distribution:
Researchers may obtain BMAP CDNA clones from RESPARCH GENETICS. It
should be noted that Bento Soares is generating a small number of
additional specialized non-redundant arrays of BMAP cDNAs whose
availability will be considered under appropriate and limited
                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 176)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                     0; Gaps
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6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85.5%; Score 18.8; DB 10; Length 176; 90.9%; Pred. No. 7.3e+02;
                                                                                                                  88.2%; Score 19.4; DB 10; Length 935; 95.2%; Pred. No. 5.7e+02; Live 0; Mismatches 1; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      collaborative arrangements
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mEST@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: M13 Reverse.
                                                                                                                                                                                                          910 CTGCCCAGGCGGAAGGCCTGG 890
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Fax: 301 443 9890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Chin, H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20892-9643, USA
                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
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Matches
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ORIGIN
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E (bases 1 to 238)

E (cono.H., Alzawa, R., Akahira, S., Akiyama, J., Arakawa, T., Carninci, Po., Endo.H., Talzawa, R., Hara, A., Hayatsu, N., Hara, A., Hayatsu, N., Hara, M., Hayatsu, N., Ishili, Y.; Ishikawa, J., Ishikawa, T., Ishikawa, J., Kikuchi, N., Izawa, M., Kadota, K., Kagwa, J., Kaya, S., Kurihara, C., Kusakabe, M., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Shipemoto, Y., Shinagawa, A., Takamura, T., Sogabe, Y., Shibata, Y., Shipata, R., Shibata, Y., Shinagawa, A., Takamashi, F., Tominaga, N., Toya, Y., Shinagawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, H., et al.)

M. Muramatsu, M. and Hayashizaki, T., Yoshida, K., Yoshiki, A., Yoshino, H., Etaloratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute

Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1.7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Hal-45-503-9226

Email: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp,
URL: http://genome.gsc.riken.
BB147701 RIKEN full-length enriched, adult female vagina Mus musculus cDNA clone 9930101123 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hiozame, T., Hori, F., Ishi, Y., Hara, A., Hayatsu, N., Lizawa, M., Kadota, K., Kagawa, J., Ishikawa, T., Itch, M., Izawa, M., Kadota, K., Kagawa, J., Kai, C., Kawai, J., Krikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, K., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, Y., Shigemoto, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watahiki, A., Yokota, T., Yamamura, T., Yamanaka, I., Yano, R., Yasuhishi, A., Yokota, T., Yamamura, T., Yamanaka, I., Yano, R., Watanishi, A., Yokota, T., Yamamura, T., Yamanaka, I., Yano, R., Konno, H., et al.)
                    BB284196 RIKEN full-length enriched, adult retina Mus musculus CDNA clone A930105B05 3', mRNA sequence.
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URL:http://genome.gsc.riken.go.jp,
carninci.p., Nishiyama,V., Westover,A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
contributed to prepare mouse tissues. 1st strand cDNA was
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For Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 393)
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Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
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Pred. No. 7.7e+02;
0; Mismatches 2; Indels 0
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90.9%;
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BB239924 RIKEN full-length enriched, 3 days neonate thymus Mus musculus cDNA clone A630079H08 3', mRNA sequence.
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                                                                                                                                                                                                                                                              /lab_host="Dilom"
/note="Site_1: Sall: Site_2: BamHI: cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project to Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKBN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAAGCATCTATTTTTTTTTTVN 3'], cDNA was
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 555)
                    Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
                                                                                                                                                                                           /clone_lib="RIKEN full-length enriched, adult retina"
/tissue_type="retina"
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Unpublished (2001)
On Jul 5, 2000 this sequence version replaced gi:8924532.
Contact: Yoshihide Hayashizaki
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                                                                                                                  /organism="Mus musculus
                                                                                                                                         /db_xref="taxon:10090"
/clone="A930105B05"
                                                                      Location/Qualifiers
                                                                                                                                                                                                                                            /dev_stage="adult"
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19-44 (1999)
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BI101919 654 bp mRNA linear EST 26-JUN-2001
602887615F1 NCI_CGAP_KId14 Mus musculus cDNA clone IMAGE:5042882
                         BH043080 608 bp DNA linear GSS 17-JUL-2001
RPCI-24 375D2.TJ RPCI-24 Mus musculus genomic clone RPCI-24-375D2,
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/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPC1-24 Mouse BAC Library produced by Pieter de Jong. The
RPC1-34 Mouse BAC Library produced by eleter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using Mbol partially digested male C57BL/6J
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Clones are derived from the mouse BAC library RPCI-24. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pdejong@mail.oho.org). Clones may be purchased from BACPAC
Resources (http://www.cho.i.org/bacpac/orderingframe.htm). BAC end
page: http://ww.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 375 row. D column: 2
Seq primer: SP6
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Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M., Tsegaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E., Russell,D., de Jong,P. and Fraser,C.M.
Mouse BAC End Sequences from Library RPCI-24
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
71: 301 838 0200
Fax: 301 838 0208
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Pred. No. 9.1e+02;
0; Mismatches 2;
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                         Email: genome-resggsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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CDNA library was prepared and sequenced in Mouse Genome consciously considered for Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
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Computational Analysis of Full-Length Mouse cDNAs Compared with
Computational Analysis of Full-Length Mouse cDNAs Compared With
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
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/db_xref="taxon:10090"
/clone="A630079H08"
/clone=lbb="RIKEN full-length enriched, 3 days neonate
+thomns"
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/dev_stage="3 days neonate"
/lab_host="DH10B"
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BF119646 959 bp mRNA linear EST 24-OCT-2000 601757514F1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:3986834 5',
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/clone_lib="NCI_CGAP_Kid14"
/lab_host="DHIOB (II_phage_resistant)"
/note="Organ: kidney; Vector: pcMv-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"
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NIH WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                            DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: LiAMIII row: n column: 03
High quality sequence stop: 654.
Location/Qualifiers
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Contact: Robert Strausberg, Ph.D.
Email: Gapbs-rémail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Theyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov.l column: 03
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Pred. No. 9.2e+02;
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/strain="C57/B6"
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Homo sapiens

Bukaryota, Metazoa: Chordata; Craniata; Vertebrata: Euteleostomi;

Mammalia: Eutheria: Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 291)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., Bordin, S., Costa, F. F., Nagai, M.A., Bordin, S., Costa, F. F., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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//dev_gatge="Adult"
//note="Organ: nervous_normal; Vector: puc18; Site_1: Smal;
Site_2: Smal; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under
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Fax: +55-11-2707001
Fax: +55-11-2707001
This solution was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM3&t2-CM3-NN0246-030101-606-d03&t3+2001-01-03&t4=1)
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                                                                    /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sal1; Sal2; NotL; Cloned unidirectionally. Primer: Oilgo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys,
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/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
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/db_xref="taxon:9606"
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Al (Dases 1 to 377)

Akimura; Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Yonno, H., Kouda, M., Matsuyama, T., Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Sakai, K., Sa
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URL:http://genome.gsc.riken.go.jp,

Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh

M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Mormalization and Subtraction of cap-trapper-selected cDNas to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

Wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,

Wathiki,M., Yooneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsurra

S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
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BB813476
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KEYWORDS
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/dec_stage="adult."
//lab_hos="adult."
/lab_hos="bH10B (life Technologies)"
/lab_hos="bH10B (life Technologies)"
/lab_hos="wettor: pT/T3D-Pac (Pharmacia) with a modified
/note="wettor: pT/T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BJOP
library is a subtracted library derived from the UI-R-BJOP
UI-R-AGI, UI-R-AGI, UI-R-AGI, UI-R-AGI, UI-R-AGI
UI-R-AGI libraries. These libraries represent tissues from
rat atrium at 16.5 dpc, ventricle at 16.5 dpc, AV canal
at 16.5 dpc, and ventricle at 13 dpc. AV canal
string of 5-6 nucleotides present between the Not I site
and the oligo-dr track. The library was constructed as
described by Bonaldo, Lennon and Soares, Genome Research
                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST 06-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: msoares@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. The sequence tag present in the cDNA between the Notl site
and the oligo-dT track served to identify it as a clone from the
normalized AV canal at 16.5 dpc library cDNA Library Preparation:
M.B. Soares Lab Clone distribution: clones will be available
through Research Genetics (www.resgen.com)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW522130
UI-R-BJOp-aga-h-02-0-UI.$1 UI-R-BJOp Rattus norvegicus CDNA clone
UI-R-BJOp-aga-h-02-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                   Gaps
                                                                                                                                                                                0;
                                                                                                                     Length 377;
                                                                                                                  Score 18.4; DB 9; Length 3;
Pred. No. 1.2e+03;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
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/clone_lib="UI-R-BJOp"
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TAG_SEQ=GAACC"
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/strain="Sprague-Dawley"
94 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Res. 6 (9), 791-806 (1996)
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91
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                                                                                                                                                                                                                                                                                                               107 GCCCGGCCGAAGGCCTGGG 126
                                                                                                                     83.6%;
                                                                                                                                                                                                                                                    3 gcccaggccgaaggcctggg 22
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265 GCCCAGGCTGAAGGCCTGGG 284
                                                                                                           house mouse.
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COMMENT
                                                      ACCESSION
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                                                                                       KEYWORDS
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                                                                                                                                                                                                                                               2059h11.1 Stratagene pancreas (#937208) Homo sapiens CDNA clone IMAGE:591237 5' similar to SW:CLP2_MOUSE Q08093 CALPONIN H2, SMOOTH AN158436
AN158436.1 GI:1733281
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1 (bases 1 to 438)

Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,White,Y., Wylie,T., Waterston,R. and Wilson,R. Theising,B., WashJr.NCI human EST Project
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 2561 Std Error: 0.00
Seq primer: -25813 rev2 from Amersham
High quality sequence stop: 392.
Location/Qualifiers
                                                                                                          Gaps
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                                                                                                        ó;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                   83.6%; Score 18.4; DB 9; Length 405; 95.0%; Pred. No. 1.2e+03; ive 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Stratagene pancreas (#937208)"
/lab_host="SOLR cells (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.6%; Score 18.4; DB 9; Length 438; 90.5%; Pred. No. 1.2e+03; ive 0; Mismatches 2; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
/clone="IMAGE:591237"
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 66
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                                                                                                                                                             316 GCCGAGGCCGAAGGCCTGGG 297
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                                                                                                      19; Conservative
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Best Local Similarity 90.5
Matches 19; Conservative
 105
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                                                                                    Best Local Similarity
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BASE COUNT
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RESULT

RESULT 13

AW553523

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//doce="Vector: pSPORT1 (Gibco/BRL Life Technology);
Site_1: Sal1; Site_2: Not1; Total RNAs were extracted from
7 NewDorn Ovary. The double-stranded cDNA was synthesized
by Gibco's kit with an Oligo(dT) primer [Not1
primer-adapter from GibcoRRL]
[5'-pGCTPACTTCAGATCCGGGCGCCCCTTTTTTTTTTTTTTT]
2.56ug of total RNA. The double-stranded cDNAs were
treated with T4 DNA polymerase and purified by
ethanol-precipitation. The cDNAs were ligated to
Lone-linker LL-Sal3 (include Sal1 sequence). The cDNAs
were purified by phenol/chloroform and separated from
free linkers by Centricon 100. Then, cDNAs were amplified
by long-range high fidelity PCR using Takara's Ex Tag
polymerase. Then, the CDNAs were purified by
phenol/chloroform and by Centricon 100. The cDNAs were
digested with Sal1 and Not1 enzymes. Then, the CDNAs were
closed into Sal1/Not1 site of pSPORT1 plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by chemical method. The library was
constructed by Xiaohong Wang and Yulan Plao."
                                                                                                                                                                                                                                                                                                             (bases 1 to 455)
Tanaka, T.S., Jardath, Muridae, Murinae, Mus.
Tanaka, T.S., Jardath, S.A., Lim, M.K., Kargul, G.J., Wang, X., Grahovac, M.J., Pantano, S., Sano, Y., Piao, Y., Nagaraja, R., Doi, H., Wood, W.H.
III, Becker, K.G. and Ko, M.S.H.
Genome-wide expression profilling of mid-gestation placenta and embryo using a 15,000 mouse developmental CDNA microarray
Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
455 bp mRNA linear EST 31-AUG-2000 L0228C11-3 NIA Mouse Newborn Ovary cDNA Library Mus musculus cDNA AW553523
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                                                                                                                                                                                                                                                         Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="niaEST:L0228C11-3"
/db_xref="taxon:10090"
/clone="L0228C11"
/clone_lib="NIA Mouse Newborn Ovary CDNA Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="female"
/dev_stage="Newborn Ovary"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plate: L0228 row: C column: 11
Seq primer: -21M13 Forward
High quality sequence stop: 455
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: George J. Kargul
                                                                                                                                                           AW553523.1 GI:7198946
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Best Local Similarity 95.0
Matches 19; Conservative
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δλ
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UI-R-CAl-bjd-j-19-0-UI.sl UI-R-CAl Rattus norvegicus cDNA clone
BF403937
    AI406571

EST234857 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone Nathorg 3, end, mRNA sequence.
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Bonaldo,M.F., Lennon,G. and Soares,M.B.

Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            451 Eckstein Medical Research Building Iowa City, IA 52242, USA Tel: 319 335 8250
Fax: 319 335 8250
Email: msoarcs@blue.weeg.uiowa.edu
The sequence contained an oligo-dT track that was present in the
                                                                                                                                                                                                                                      1 (bases 1 to 512)
Lee.N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Normalized rat kidney, Bento Soares"
/note="Organ: kidney; Vector: pT/T3Pac; Site_1: EcoRI;
Site_2: Not1"
in 135 c 137 g 124 t
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                                                                                                                                                                                                                                                                                                                                                            Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
701: (301)-838-3529
Fax: (301)-838-0208
Email: nhleetigr.org
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Program for Rat Gene Discovery and Mapping
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/clone="RKIDY92"
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// Actains | Sprague-Dawley |
// Actor | Sprague-Dawley |
// Actor | Sprague-Dawley |
// Actor | Sprague-Dawley |
// Clone | 1b="UT-R-CAl-bjd-j-19-0-UI" |
// Clone | 1b="UT-R-CAl-bjd" |
// Alab_host="DH10B (Life Technologies)" |
// Alab_host="WetOr: pT730-Pace (Pharmacia) with a modified |
// Actor | PT730-Pace (Pharmacia) with a modified |
// Actor | PT730-Pace (Pharmacia) with a modified |
// PACAL | Ibrary | Site_1: BCO RI; The UI-R-CAl |
// Actor | Site_1: Not I; Site_2: ECO RI; The UI-R-CAl |
// Actor | Ibrary | Site_1: Not I; Site_2: ECO RI; The UI-R-CAl |
// Actor | Ibrary |
// Actor | Ibrary |
// Actor | Actor | Actor |
// 
oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bonafide poly A tail. The sequence tag present in the cDNA between the NotI site and the oligo-dr track served to identify it as a clone from the normalized thalamus library cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research
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ilarity 95.0%; Pred. No. 1.3e+03;
Conservative 0; Mismatches 1;
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Job time: 7506 sec
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TAG_TISSUE=thalamus
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Perfect score:

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AC011969 H AC006558 H

AC073464 Homo sapi AL137070 Human DNA

6 Mus muscu Human DNA

Sequence

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AP001078 Homo sapi AP001793 Homo sapi AC015676 Homo sapi AF020899 Homo sapi AF32875 Bradyrhiz AF11965 Pseudomon AF153207 Pseudomon

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gode,W., Becker,D., Randles,J.W., Hehn,A. and Salamini,F.

Use of a virus DNA as promoter

Patent: US 6303345-A 6 16-0CT-2001;
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Copyright (c) 1993 - 2000
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E01204 DNA sequence AR16888 Sequence AX10137 Sequence AR168887 Sequence AX015319 Sequence

AF023257 Mus muscu

AX015318 Sequence AX166558 Sequence

PAT 17-DEC-2001

No.

184559 Sequence 1 U81984 Human endot AR108902 Sequence AX101372 Sequence AX101372 Sequence

AX101354 Sequence

AX230581 Sequence

AK026727 Homo sapi BC013149 Homo sapi D83735 Homo sapien AK024835 Homo sapi AX015317 Sequence

δ g

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On Jun 27, 2001 this sequence version replaced gi:14270608. On Jun 27, 2001 this sequence version replaced from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL513122 108930 bp DNA linear PRI 26\text{-JUN-}2001 Human DNA sequence from clone RP11-477J21 on chromosome 9, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAA42899.1"
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                                                                                                                                                                                                                                                                                                                                                 /translation="MRTRRREVRVCQISRTQARLVLHMWNQKGRIVPVHRGPKTKFNPRCTQV"
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                                                                                                                                                                                                                              /translation="MEMGTDFQRPILSIPPKLRVQRIFGIRLGLPGGVHQVPQQIVGP
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (26-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1291;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAA42898.1"
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/db_xref="GI:323308"
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/note="ORF 5"
                                                                                                                                complement(422. .568)
/note="ORF 6"
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/note="ORF 4"
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Laird, G.
                    /codon_start=1
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/note="ORF 2"
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LEVLSAIGEPADDRTILMLGGROGGOGKSYPAKYLGLKPDMFYTGGGTRKDVLXQYIE
DPKRNLILDVPRCNLEYLNYALLECVKNRAFSSDKXEPLSYLGFDHVHVLVFANVLPD
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Coconut foliar decay virus DNA, clones NMORG, poRG, and pORGSAUJA..

Coconut foliar decay virus

Viruses; ssDNA viruses;

(bases 1 to 1291)

(coconut foliar decay, Nanovirus)

Nucleotide sequence of a circular single-stranded DNA associated with coconut foliar decay virus
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                                                                                                                                                                                                                                                                                                                                         (Asses 1 to 1291)
Rohde, W., Becker, D., Randles, J.W., Hehn, A. and Salamini, F. Use of a virus DNA as promoter
Patent: US 63345-A 1 16-OCT-2001;
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Draft entry and printed sequence for [1] kindly subm
W.Rhode, 15-MAR-1989, for release after publication.
Location/Qualifiers
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        Indels
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                                                                                                                                                                                     DNA
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103. ,975
          Mismatches
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                                                                                                                                                                                   AR172770 1291 bp
Sequence 1 from patent US 6303345.
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314. .775
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                                            1 ctgcccaggccgaaggcctggg 22
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Matches 22; Conserv
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Gaps

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matches 220.

This sequence was finished as follows unless otherwise noted: all regions were either double stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone, and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, database can be found at http://www.sanger.ac.uk/Projects/C\_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human crhomosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Croup. Purther information can be found at http://www.sanger.ac.uk/HGPP/Chr9 RPP11-477321 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see http://www.chri.org/bacpac/home.htm IMPORTANT: This sequence is not the entire insert of clone RP11+47721 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true right end of clone RP11-47721 is at 108930 in this sequence. The true left end of clone RP11-342H3 is at 29985 in this sequence. The true right end of clone RP11-165P4 is at 100 in this 5296 .5413 . ---- matches 4908 .5022 of consensus" 5414 .5637 . ---- matches 1 .216 of consensus" 5638 .598 .5980 1973. .2675 //note="LiMC4 repeat: matches 6783. .7492 of consensus" 1187. .1672 /note="LiMC4 repeat: matches 7492. .7975 of consensus" 5008. .5134 /note="LiMB1 repeat: matches 6042. .6168 of consensus" 5296. .5418 5210. .6327 /note="HERVL repeat: matches 4794. .4908 of consensus" 9941. .6209 /note="MLTIG repeat: matches 216. .510 of consensus" 605. .725 /note="L2 repeat: matches 2624. .2746 of consensus" /note="MER21B repeat: matches 6. .201 of consensus" repeat: matches 2589. .2710 of consensus" 379. .1178 note="AluJb repeat: matches 1. .309 of consensus" 1673. 1972 /note="Alusx repeat: matches 1. .304 of consensus" 1252. .4523 /note="AluSg repeat: matches 1. .283 of consensus" 638. 5940 note="Alusg repeat: matches 1. .302 of consensus" 328. 6781 /note="MLTlJ repeat: matches 1. .516 of consensus" 3053. .3202 /note="MIR repeat: matches 82. .248 of consensus" /organism="Homo sapiens" /clone\_lib="RPCI-11.2" 1. .187 /db\_xref="taxon:9606" /chromosome="9" /clone="RP11-477J21" Location/Qualifiers 4641. .4753 /note="L2 re 5008. .5134 .108930 pBACe3.6 1973. sednence repeat\_region source

FEATURES

note="HERVL repeat: matches 4402. ,4794 of consensus"

7153

repeat\_region repeat\_region repeat\_region repeat\_region

8178. .8363 /note="MLT1J repeat: matches 1. .200 of consensus" 8396. .8634

note="FRAM repeat: matches 1. .158 of consensus"

27703. .27989 /note="AluJb repeat: matches 1. .295 of consensus" 28105. .28317 /note="LIMC/D repeat: matches 5617. .5822 of consensus" //note="LiMC/D repeat: matches 5704. .5810 of consensus" 17803. .18108 15446. .15938 /note="MLT1D repeat: matches 1. .502 of consensus" 16000. .16056 /note="L1ME1 repeat: matches 6105. .6162 of consensus" 16057. .16331 /note="LimEl repeat: matches 5442. .6105 of consensus" 17094. .17197 /note="FAM repeat: matches 1. .159 of consensus"
18400. .18716
/note="Limc5 repeat: matches 7610. .7925 of consensus"
2037. .2018/x repeat: matches 140. .291 of consensus"
2039. .21587 28758. .29049 /note="L1MA4 repeat: matches 5769. .6074 of consensus" 29373. .29603 . /note="LiMA4 repeat: matches 6074. .6300 of consensus" .466 of consensus" /note="L1 repeat: matches 4205. .4658 of consensus" 13905. .14075 /005e\_\_11887 /006e\_"L2 repeat: matches 1949. .2748 of consensus." 21631. .21947 /006e\_"Aluby repeat: matches 1. .299 of consensus." 22652. .22056 /006e\_"Alusg repeat: matches 1. .305 of consensus." 23007. .23286 /note\_"Alusg repeat: matches 5. .283 of consensus." /note="AluSq repeat: matches 1. .305 of consensus" 24478. .24527 /note="L2 repeat: matches 2698. .2747 of consensus" 24643. .24880 24643. .24880 /note="L2 repeat: matches 2248. .2476 of consensus" 24954. .25299 /note="MLTIL repeat: matches 68. .410 of consensus" 75300. .25344 /note="L2 repeat: matches 2197. .2235 of consensus" 25345. .25707 /note="Mirial repeat: matches 1. .365 of consensus" 25708. .25752 7.04ce="L2 repeat: matches 2151. .2197 of consensus" 27394. .27701 7.00ce="Alux repeat: matches 1. .309 of consensus" 8664. .8966 /note="AluSg repeat: matches 1. .308 of consensus" /note="AluJb repeat: matches 1. .304 of consensus" 10611. .11123 /note="MLT2B repeat: matches 1. .448 of consensus" 12545. .12786 repeat: matches 1. .229 of consensus" /note="AluSq repeat: matches 1. .275 of consensus" /note="AluJo repeat: matches 7. .308 of consensus" 18212. .18370 .250 of consensus" /note="AluSx repeat: matches 1. .298 of consensus" 24131. .24437 29050. 29372 /note="AluSq repeat: matches 1. .311 of consensus" Jobus. .14075 /note="MIR repeat: matches 50. .216 of consensus" 14560. .14653 /note="MIR repeat: matches 152. /note="MLT1C repeat: 13855 17014 16331 /note="MLT1C 13425. .13855 repeat\_region repeat\_region

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F31326 Castanet-Tolosan Cedex. Laboratoire de Genetique Cellulaire
                 INRA, BP27, F31336 Castanet Tolosan Cedex
Christian Boucher@toulouse.inra.fr
http://sequence.toulouse.inra.fr/solanacearum.html.
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/functe="Product confidence : hypothetical
dene name confidence : hypothetical
predicted by Codon_usage
predicted by FrameD"
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Gene name confidence : hypothetical
predicted by Codon_usage
predicted by Homology
predicted by FrameD"
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Gene name confidence : hypothetical
predicted by Codon_usage
predicted by Homology
predicted by FrameD"
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                                                                                               Location/Qualifiers
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789. .1517
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                                                                                                                                                                /strain="GMI1000
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                                                                                                                                                                                                                                     /gene="RSc0962"
                                                                                                                                                                                                                                                           note="RS04402"
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(bases 1 to 193050)

alanoubat,M., Genin,S., Artiguenave,F., Gouzy,J., Mangenot,S., Arlat,M., Billault,A., Brottier,P., Camus,J.C., Cattolico,L., Chandler,M., Choisne,N., Claudel-Renard,C., Cunnac,S., Demange,N., Gaspin,C., Lavie,M., Moisan,A., Robert,C., Saurin,W., Schiex,T., Siquier,P., Thebault,P., Whalen,M., Wincker,P., Levy,M., Weissenbach,J. and Boucher,C.A.
Genome sequence of the plant pathogen Raistonia solanacearum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35560. 35847
/note="WER63B repeat: matches 1. .278 of consensus"
35848. 36062
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36063. 36363
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/note="L2 repeat: matches 2243. .2508 of consensus" 33093. .33156
/note="Mir repeat: matches 86. .151 of consensus" 33876. .34052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anote="MIR repeat: matches 20. .262 of consensus" 35373. .3551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MIR repeat: matches 98. .194 of consensus" 34707. .34926
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                                  .262 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88.2%; Score 19.4; DB 9; Length 108930; 95.2%; Pred. No. 3.7e+02;
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29964. .30044
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30668. .30932
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AL646062.1 GI:17427974
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Boucher, C.A.
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AL646062/c
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VRTLSPSSYPDPEVARQLAGRSEPVAHAV"
2400. 2576
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REGULATOR PROTEIN"
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function="elements of external origin; phage-related
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Baldwin, J., Barnan, M., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barnan, N., Beckerly, R., Boquslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FizzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., McDean, P., McGurk, A., McKernan, K., McLaughlin, J., Marquis, N., McKernan, K., McLaughlin, J., Marquis, N., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollarav, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
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Letvarloqorcsavfryavytgraahnpctdlkgafktakvqhmarvqanevptlikn
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193168 bp DNA linear HTG 21-APR-2000
HOMO Sapiens chromosome 4 clone RP11-520J8 map 4, WORKING DRAFT
SEQUENCE, 13 unordered pieces.
                                                                             /function="elements of external origin; transposon-related functions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IRGYDGDL ITRIALQFWALTFVRTKEL IGAOWSEIDFETEEWRIPAERKKMREPHFVP
LSWQAIALLRAAEKMTGNRQYVFQSPKGRTHISNNTILYALYRLGYHSRWTGHGFRGL
ASTWLHEQGFNPDVIERQLAHAERNKVRAAYNHAQYLPERRRWMGHWADHLDQLAQD"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 4, clone RP11-52038
                                                                                                                                           /note="Product confidence : probable
                                                                                                                                                                    Gene name confidence: hypothetical predicted by Codon_usage predicted by Homology predicted by FrameD**
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/gene="tRNA-argw"
                      complement(6298. .7473)
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Gaps

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δλ
Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                           Consensus quality: 126832 bases at least Q40 consensus quality: 155745 bases at least Q30 consensus quality: 175228 bases at least Q30 consensus quality: 175228 bases at least Q20 Insert size: 186000; agarose-fp Insert size: 191968; sum-of-contigs Quality coverage: 3.2 in Q20 bases; agarose-fp Quality coverage: 3.1 in Q20 bases; sum-of-contigs
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Center clone name: 520_J_8
Sequencing vector: M3: M7815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
                                                                             Contact: sequence_submissions@genome.wi.mit.edu
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69586 99210: contig of 29625 bp in length
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Sirren, B. Linton, L. Barna, N., Beckerly, R., Bann, J., Brown, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Depayre, E., Devon, K., Dewar, K., Donelan, L., Doyle, M., Ferreira, P., Fitzhugh, M., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G., Raratas, A., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stone, C., Subramanian, A., Tesfaye, S., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wuy, X., Wayman, D., Ye, W.J. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACO06558 207392 bp DNA linear HTG 10-FEB-1999 Homo sapiens chromosome 9 clone hRPK.477_J_21 map 9, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (10-FEB-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 207392)
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* NOTE: This is a 'working draft' sequence. It currently
* consists of, contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* truns of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 19.4; DB 2; Length 193168;
Pred. No. 3.1e+02;
0; Mismatches 1; Indels 0;
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95.2%;
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Best Local Similarity 95.2%
Matches 20; Conservative
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TEAIARALLNHRNLKIITNNLHVAATLSAKEDFEVLVAGGTVRSDGGIVGQAAVDFIQ
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RPHLRPAWMIRAGLFLYDHLGKREKLPASRGLRFTGSSPLKAEIRRGFEYSDCAVDDA
RLVVLNAISAREHGAHVHTRTRCVSARRSKGLWHLHLBRSDGSLYSIRARALVNAAGP
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MIGTTDREVGGSPARVAISEEETAYLLQWUNHFKQOLAAADILHSFRGVRPLCDDES
BESAITRDYLSLSAGGREPLLSVEGGKLTYRKLAESALTQLQPFFANLGPAWTA
KAPLPGGEQMOSVELLTEQLANKYAWIDRELALKWARTYGTRWRLLDGVNGFADLGE
HLGGGLYAREVDYLCKHEWAQDAEDILMRRSKLGLFLSPSQQVRLGGYLGSEHPHRPR
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163. .1002
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/note="PA3584"
3798, .5336
                                                                                      /note="PA3581"
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                                                                                                                                   /gene="glpF"
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/gene="glpD"
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/gene="glpM"
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Stover, C.K., Pham, X.O., Erwin, A.L., Mizoguchi, S.D., Warrener, P.,
Hickey, M.J., Brinkman, F.S., Hufnagle, W.O., Kowalik, D.J., Lagrou, M.,
Garber, R.L., Goltry, L., Tolentino, E., Westbrock-Wadman, S., Yuan, Y.,
Brody, L.L., Coulter, S.N., Folger, K.R., Kas, A., Larbig, K., Lim, R.,
Smith, K., Spencer, D., Wong, G.K., Wu, Z. and Paulsen, I.T.
Complete genome sequence of Pseudomonas aeruginosa PA01, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stover, C. K., Pham, X.—Q.T., Erwin, A. L., Mizoguchi, S. D., Warrener, P., Hickey, M. J., Brinkman, F. S. L., Hufnagle, W. O., Kowalik, D. J., Lagrou, M., Garber, R. L., Goltry, L., Tolentino, E., Westbrook Wadman, S., Yuan, Y., Brody, L. L., Coulter, S. N., Folger, K. R., Kas, A., Larbig, K., Lim, R. M., Smith, K. A., Spencer, D. H., Wong, G. K. S., Wu, Z., Paulsen, I. T., Reizer, J., Saier, M. H., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (16-MAY-2000) Department of Medicine and Genetics, University of Washington Genome Center, University of Washington, Box 352145, Seattle, MA 98195, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AE004779 15982 bp DNA linear BCT 30-AUG-2
Pseudomonas aeruginosa PA01, section 340 of 529 of the complete
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                                                                                                                                                                                                                                               gap of unknown length
87103: contig of 30931 bp in length
gap of unknown length
007392: contig of 120289 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="hRPK.477_J_21"
/clone_lib="RPCI-11 human BAC library"
44607 c 45345 g 58166 t 1283 others
                                                                                                gap of unknown length
24168: contig of 14536 bp in length
gap of unknown length
                                                                                                                                                                                               gap of unknown length
56172: contig of 17806 bp in length
                                                                                                                                                                      contig of 14198 bp in length
                                             gap of unknown length
9632: contig of 6319 bp in length
                     of 3313 bp in length
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                                                                                                                                                                                                                                                                                                                                                                           1. .207392
/organism="Homo sapiens"
/db_xref="taxon:9606"
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Nature 406 (6799), 959-964 (2000)
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                  3313: contig
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Best Local Similarity 95.28
Matches 20, Conservative
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preserved
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Direct Submission
Submitted (18-JUN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                      LERÖLEEVVGÜEALLASNTSSLSVTATASACRDPGRIAGLHFRNPVPLMRLVEVIEGL
BYLRGJAERLCALVAFFGHQAYRATDESGETVINHAGRARGTEALRILGESVAPVAAID
EVLREGAGFRUGPFELFDLVGLDVSLPVMESIYROYYEEPRYRPHPLIROMLAGRIG
RKSGGGFYRYDGAGOVPVAAAPVAPGAALPPVWLGVDDEHDRAPLLMLLQRLGAEVES
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Submitted (26-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
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                                                                                                                                                                                                                                                                                                       /traislation="MSEPSIVLIGIVGTGAMGQGIAQLAACAGLSVLLYDSRQGVALQ
AREQIATVLARQVERGRLEAEAVERAMGNLRVVEDLRVLGGCQLVIEAIVENLEAKQA
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PLARILASASVGVEPRLMGIGPQQAILRALQRAGIDLDEVGLIEINEAFAPQVLACLK
LLGLDYEDPRVNPHGGAIALGHPLGASGARLVLTAARGLQRIERRYAVVSLCVGLGQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens BAC clone RP11-134N21 from 2, complete sequence. Ac073464
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Submitted (09-JAN-2002) Department of Genetics, Washington Submitted (09-JAN-2002) Department of Genetics, Missouri 63 University, 4444 Forest Park Avenue, St. Louis, Missouri 63 On Sep 26, 2001 this sequence version replaced gi:15487456.
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Center code: WUGSC
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Shah,N., Cotton,M. and Boyer,E.
The sequence of Homo sapiens BAC clone RP11-134N21
Unpublished (2001)
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100.0%; Pred. No. 9.6e+02;
.ive 0; Mismatches 0; Indels
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Contact: sapiens@watson.wustl.edu
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Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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                                                                                 complement(10557. .12089)
                                                                                                                                     complement(10557. .12089)
                                                                                                                                                                                                                                   /product="probable hydrox
/protein_id="AAG06978.1"
/db_xref="G1:9949745"
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/transl_table=11
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Waterston, R.H.
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5 (bases 1 to 168862)
Waterston, R.
                                                                                                                                                             /gene="PA3590"
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Waterston, R.H.
                                                                                                           /gene="PA3590"
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                                                              VAMVIERCR"
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Matches 19; Conservative
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CELSGLSLNLGRLTFVSQRNRAGTSDLALFNRNRRAGAAQADRFDLAGLDYRIAPDM
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SMPETGDNVARAFGTAREDADRFAASSQASKYGAALEEGFFLGEILPVEVRAGRKGFTR
LVERDEHPRPQADLAALARLPALFAGGVYTAGNASGINDGAAVVLLGDRAIGEREGIR
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RQOLLLQAARSYDRAFNPEGVQRQLLAILAEPSRVPLLNRLQVPTLYIHGTADPLLPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GMQLEVRKTKPVRFTSAGLRLLQLADSLLPQLRTAERPLARLAGGTAGRLHMA I ECHS
CFQWLMTIDQFRDAMPEVELDLASGFSFAPLPALARGDLDLVVTADPVELPGITYVP
LFTYEALLAVANQHALAGRPYVVPEDLERETLITYPVERDRLDVFTRFLDPADVEPAQ
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complement(5815. .6801)
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc

## SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
(http://bacpac.med.buffalo.edu)

# NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RP11-71B7. Actual start of this clone is at base position 1 of RP11-134N21; actual end is at base position 168862 of RP11-134N21.

Data from AC068165 and AC092432 was used to finish this clone, AC073464.

### FEATURES

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Direct Submission

Direct Submission

Direct Submission

Submitted (04-DEC-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CBIO 15A, UK. E-mail enquiries:

humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

on Jul 22, 2000 this sequence version replaced gi:8977609.

During sequence assembly date is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission colly a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL; Sw.: SMISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.sanger.ac.uk/FGP/Chr9

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by thigh quality data (1.e., phred quality) as compressions and repeats; all regions were covered by at least one planning was confirmed by resolve all sequencing problems, such as campressions and repeats; all regions were covered by at least one planning subclone or more than one Mill subclone; and the assembly was confirmed by resolve all sequencing problems, such the library RPCI-II.1 constructed by the group of Pieter de Jong. For the Library RPCI-II.1 constructed by the group of Pieter de Jong.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AL137070 Human DNA sequence from clone RP11-251017 on chromosome 9 Contains 2 calponin 2 (CNNZ) pseudogenes, a gene for a novel protein similar to aduaporin 7 (AQP7), part of gene for a novel protein similar to methylenetetrahydrofolate dehydrogenase(NADP+ dependent), methenyltetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthetase (MTHFD1) and a CPG island, complete sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 170237)
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Pred. No. 4.6e+02;
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VECTOR: pBACe3.6.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           100.0%; Pred. No. 4.6 ive 0; Mismatches
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31807. .31839
/rpt_family="AT_rich"
32015. .32038
                   /rpt_family="AT_rich"
29984, .30783
                                                                                 /rpt_family="L1"
30871. .31273
                                                                                                                                          /rpt_family="L1"
31261. .31285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 65377 GCCCAGGCCGAAGGCCTGG 65395
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           29506. .29537
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Matches 19; Conserv
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TITLE

VERSION SOURCE

δλ

COMMENT

.170237

source

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2090. .2613
/note="LIPB2 repeat: matches 5614. .6155 of consensus"
complement(2326. .3058)
/note="match: GSS: Em:AQ78000"
complement(2332. .3081)
/note="match: GSS: Em:AQ749938"
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/note="L1M4 repeat: matches 5352. .5586 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .564 of consensus"
                                                                                                                                  92. .384
/note="AluJo repeat: matches 1. .288 of consensus"
                                                                                                                                                                              1467. .1634
/note="2 copies 84 mer 81% conserved"
2090. .2613
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/note="match: GSS: Em:AQ810980"
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3155, .3616
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3088. .3353
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/note="match: GSS: Em:AQ493601"
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note="match: GSS:
                                                                                                                                                                 complement(527
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                                            .564
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4520. 4733
Anote="MERAO repeat: matches 1. 230 of consensus" complement(4614. 5113)
Anote="match: GSs: Em: A0547317"
Complement(4616. 5130)
Anote="match: GSs: Em: A0380868"
Complement(4616. 5127)
Anote="match: GSs: Em: A0748099"
Complement(4616. 5127)
Anote="match: GSs: Em: A0748099"
Complement(4616. 5127)
Anote="match: GSs: Em: A0682825"
Complement(4610. 5373)
Anote="match: GSs: Em: A0194341"
                                                                                                                                                                                                                                                                                                                                                                              .426 of consensus"
4398. .4519
/note="MSTB repeat: matches 1, .121 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .282 of consensus"
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/note="match: GSS: Em:AQ178179"
complement(join(6671, .7023,7998, .8098))
/note="match: GSS: Em:AQ278128"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(6703..7023,7998..8166))
/note="match: GSS: Em:AQ571063"
complement(6772..7032)
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// note="match: GSS: Em:AQ269571"

4734. 5035

// note="match: GSS: Em:AQ469571"

// note="match: GSS: Em:AQ418853"

// note="match: GSS: Em:AQ418853"

// note="match: GSS: Em:AQ4594"

// note="match: GSS: Em:AQ4594"

// note="match: GSS: Em:AQ4554"

// note="match: GSS: Em:AQ45575"

// note="match: GSS: Em:AQ4555"

// note="match: GSS: Em:AQ346755"

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// note="match: GSS: Em:AQ346755"

// note="match: GSS: Em:AQ34010"

// note="match: GSS: Em:AQ34010"

// note="match: GSS: Em:AQ34010"
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/note-*Aludo repeat: matches 1.
5793. 5946
/note-"match: GSS: Em:AQ520858"
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/note="match: GSS: Em:AQ409721"
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/note="match: GSS: Em:AQ798688"
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5381. .5493
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5386. .5658
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5389. .5789
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'note="match: GSS: Em:AQ808738"
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/note="match: GSS: Em:AQ232792"
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6902. .7238
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complement(6419. .6895)
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5450, .5792
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae; Lo 2540)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIAL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                Gaps
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Leach,M.D. and Shimkets,R.A.
Human polynucleotides and polypeptides encoded thereby
Patent: WO 0190366-A 8343 29-NOV-2001;
                                                                                                     Length 170237;
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85.5%; Score 18.8; DB 6; Length 324;
Best Local Similarity 90.9%; Pred. No. 3.8e+03;
Matches 20; Conservative 0; Mismatches 2; Indels
                                                                                                                                            0; Indels
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Contact: MGC help desk
                                                                                                   86.4%; Score 19; DB 9; L 100.0%; Pred. No. 4.6e+02;
/note="match: GSS: Em:AQ770277"
6987. .7346
                                      /note="match: GSS: Em:AQ228275"
7030. .7997
                                                                                                            100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                     324 bp Di
Sequence 8343 from Patent W00190366,
AX315358
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/db_xref="taxon:9606"
84 c 89 q 69
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Location/Qualifiers
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BC011256.1 GI:15030027
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                                                                                         Query Match
Best Local Similarity 100.0
Matches 19; Conservative
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RRPNALKLGIGONHNYCRNPDRPILKPWOYVEKAGKYTTEECSTPACPKGKSEDCYVGKG
VTYRGTHSLTTSQASCLPWNSIVLMGKSYTAWRTNSQALGLGRHNYCRNPDGDARPWC
HVMKDRKLTWEYCDMSPCSTCGLRQYKRPOFRIKGGLYTDISHPWOARLIFVKNKRSP
GERFLCGGVLISSCWVLSAAHCFLERPPNHLKVVLGRTYRVYGEBEGTFEIEKYIV
HEBENDDAYDNDIALLQLRSOSKOCAQESSSVGTACLPDPNHQLPDWTECELSGYGKH
EASSPFFSDRLKEAHVRLYRSSKCTSQHLFNKTVTNNMLCAGDTRSGGNQDLHDACOG
DSGGPLYCMINKQMTLTGIISNGLGCGCQRDVFGVYTKVTNYLDWIHDNMKQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="WKRELLCVLLLCGLAFPLPDQGIHGRFRRGARSYRATCRDEPTQ
TTYQQHQSWLRPMLRSSRVEYCRCNSGLVQCHSVPVRSCSEPRCFNGGTCQQALXFSD
FVCQCPDGFVGKRCDIDTRATCFEEQGITYRGTWSTAESGAECINWNSSVLSLKPYNA
                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 24 Row: d Column: 24 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 202109.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="Mammary tumor. WAP-TGF alpha model. 7 months
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During sequence assembly data is compared from overlapping clones.
                   Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., Lu, X., Garcia,
Villalon, D.K., Telford, B, Hodgson, A., Bouck, J., Yu, W.,
Muzny, D.M., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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Pred. No. 2e+03;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="MGC:18508 IMAGE:4038404"
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/clone_lib="NCI_CGAP_Mam5"
/lab_host="DH10B"
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/db_xref="G1:15030028"
                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
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Almeida, J.
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Matches 20; Conservative
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/evidence=not_experimental
join(1846. .1956,21132. .21252,22789. .22831,23186. .23288,
24093. .>24191)
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Em:J03023 Em:M16592 Em:M85666 Em:Y00487 Em:X60380
Em:J03579 Em:X67796 Em:AF000300 Em:AF000301 Em:AF000302
Em:M17031 Em:X2822 Em:X57018 Em:X1545 Em:M27454
Em:M57290 Em:X57684 Em:M85043 Em:M1972
where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="MER20 repeat: matches 26. .218 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110. .586
Thote="12 repeat: matches 1966. .2045 of consensus"
692. .906
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1576. .2453
/note="CpG island"
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/note="match: GSS: Em:AQ382576"
complement(2108. .2557)
/note="match: GSS: Em:AQ461389"
complement(2196. .2570)
/note="match: GSS: Em:AQ240986"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(39. .567)
/note="match: GSS: Em:AQ386884"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2.
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/db_xref="taxon:9606"
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/gene="HCK"
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7866. 5115
7001e="LiMC1 repeat: matches 57. 572 01 consensus"
7004e="LiMC1 repeat: matches 5725. 5980 of consensus"
5124. 5701
7004e="LiMB5 repeat: matches 5615. 6171 of consensus"
5702. 5999
7004e="AluY repeat: matches 1. 295 of consensus"
6000. 6157
7006="LiMB5 repeat: matches 5454. 5615 of consensus"
6276. 6318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10208. .10442
/note="LTR16B repeat: matches 250. .459 of consensus"
1043. .10751
/note="Alusg repeat: matches 1. .309 of consensus"
10752. .1095
/note="LTR16B repeat: matches 2. .250 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                     3809. .3976
/note="AluSp repeat: matches 147. .313 of consensus" 3997. .4296
/note="AluY repeat: matches 3. .302 of consensus"
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/note="L2 repeat: matches 2623. ,2730 of consensus"
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Anote="12 copies 2 mer ac 97% conserved"

8139. .8510

Anote="LTR16C repeat: matches 1. .387 of consensus"
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/note="L2 repeat: matches 2157. .2577 of consensus"
complement(11015. .11870)
                                                                                                                                                                                                                                                                                                                         /note="MIR repeat: matches 193. .252 of consensus"
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/note="AluJb repeat: matches 1. .299 of consensus" 7087. .7147
/note="Min repeat: matches 68. .133 of consensus" 7614. .77706
                                                                                                                                                                                                                                                             2826. 3131
/note="Alusx repeat: matches 1. 306 of consensus"
                                                                                                                                                                                                                                                                                                                                                   /note="MERSA repeat: matches 1. .184 of consensus" 3809. .3976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anote="MIR repeat: matches 47. .140 of consensus" 7720. 8014
Alusq repeat: matches 1. .297 of consensus"
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/note="MIR repeat: matches 76. 193 of consensus"
                 'note="MIR repeat: matches 89. .148 of consensus"
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/note="48 copies 4 mer cttc 62% conserved"
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/note="75 copies 2 mer tt 60% conserved"
88795. .8974
/note="5 copies 36 mer 68% conserved"
8820. .8957
/note="46 copies 3 mer ct 66% conserved"
                                                                              'note="match: GSS: Em:AQ201482"
1576. ,3351
                                                                                                                                        /note="match: GSS: Em:AQ748323"
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8076. .8119
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/note="match: GSS: Em:AQ896828"
                                      2575. .3113
/gene="HCK"
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/gene="HCK"
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/gene="HCK"
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Hattori,M., Ishi,K., Toyoda,A., Taylor,T.D., Hong-Seeg,P., Fuliyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Homo sapiens 176,253 genomic DNa of 18pll.3
Published Only in DataBase (2000) In press
1 to 176253)
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fuliyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
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Homo sapiens chromosome 18 clone RP11-861B19 map 18p11.3, WORKING
BRAFT SEQUENCE, 26 unordered pieces.
AP001078
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                                                                                                                                           /note="L2 repeat: matches 2132, .2157 of consensus" 11890. .12417 /gene="HCK"
              /note="AluSx repeat: matches 3. .303 of consensus" complement(11415. .11855) /note="match: GSS: Em:AQ369535" complement(11468. .11868)
                                                                                                                                                                                                                                                                                                                  12733. .13018
/note="AluJo repeat: matches 1. .292 of consensus"
13463. .13759
                                                                                                                                                                                                                                                                                                                                                                             note="AluSx repeat: matches 5. .311 of consensus"
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                                                                                                           /note="match: GSS: Em:AQ709950"
/note: 11708 . 11734
                                                                                                 /note="match: GSS: Em:AQ135725"
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                                                                                                                                                                                                                                                                                                   /note="match: GSS: Em:AQ419051"
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11920. .12309
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Homo sapiens DNA, clone:RP11-861B19.
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Matches 20; Conservative
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/note="assembly_fragment clone_end:SP6 vector_side:left"
                                                  111290: gap of 100 bp 111290: gap of 100 bp 118174: gap of 100 bp 11240: gap of 100 bp 112936: contig of 5838 bp in length 12936: contig of 5537 bp in length 135210: gap of 100 bp 135210: gap of 100 bp 14146: contig of 5936 bp in length 14146: gap of 100 bp 14536: gap of 100 bp 15092: gap of 100 bp 15092: contig of 4312 bp in length 15092: contig of 4338 bp in length 155230: contig of 4338 bp in length 15530: gap of 100 bp 155230: contig of 4338 bp in length 158860: gap of 100 bp 168860: gap of 100 bp 168880: gap of 168880: gap 
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99847. 105997
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91096. .99746
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/db_xref="taxon:9606"
                   105998 106097: gap of
106098 112950: contig of
112951 113050: gap of
113051 118074: contig of
                                                                                                     118075 118174: gap of 118175 124012: contig of
105997: contig of
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                                                                                                                                               .24013 124112: gap of
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                                                                                                                                                                                                                                                                                                                                                                    26 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence preserved.
                                                                                                          Center project cane: Humbrating
Center clone name: RP11-861B19
Center clone name: RP11-861B19
Center clone name: RP11-861B19
Center clone name: RP11-861B19
Sequencing vector: PCR products; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 15578 bases at least Q40
Consensus quality: 165815 bases at least Q30
Consensus quality: 17632 bases at least Q20
Insert size: 173753; sum-of-contigs
Quality coverage: 4.13x in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently consists of 26 contigs. The true order of the pieces is not known and their order in this sequence record is
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                                                  Web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
------ Project Information
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Homo sapiens chromosome 18 clone RP11-661013 map 18p11.3, WORKING DRAFT SEQUENCE, 32 unordered pieces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EuKaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 193487)
Hattori,M., Ishi,K., Toyoda,A., Taylor,T.D., Hong-Seog,P. Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Published Only in Database (2000) In press
C bases 1 to 193487; Danabase (2000) In press
Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
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Fax:81-42-778-9924)
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Contact: hattori@gsc.riken.go.jp
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/note="assembly_fragment"
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Contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be
                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence updated (26 May-2000).

* NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will
Sequencing vector: PCR products; 100% of reads Chemistry: Dye-terminator ET-amersham; 100% of reads Assembly program: Phrap; version 0.990329 consensus quality: 176668 bases at least 040 consensus quality: 185034 bases at least 040 consensus quality: 18618 bases at least 020 Insert size: 190887; sum-of-contigs Quality coverage: 4.33x in 020 bases; sum-of-contigs
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3692 bp in length
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3874: gap of 100 bp

149669: contig of 5795 bp in length

49769: gap of 100 bp

13769: gap of 3767 bp in length
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190762 191967: contig of 1206 bp in length
191968 192067: gap of 100 bp
192068 193487: contig of 1420 bp in length.
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158023: contig of 4387 bp in length
8123: gap of 100 bp
162445: contig of 4322 bp in length
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Troubles of Wild Man	CFDV-DNA fragment CFDV-DNA fragment Human ORFX ORF880 Human secreted pro Human musculoskele Human FATP alterna Human hydrolase ho Pseudomonas aerugi											
SUMMARIES		OI (	AAX02689	AAX02687	AAC75325	AA227241	AAL34910	AAZ38123	AAZ49239	AAS54242	AAS06749				
		B	20	20	21	20	22	20	21	23	22				
	Query	Length	44	44	324	1592	313	496	524	807	834				
ص	Query	Match	100.0	100.0	85.5	85.5	80.9	80.9	80.9	80.9	80.9				
	·	score	22	22	18.8	18.8	17.8	17.8	17.8	17.8	17.8				
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AAL01852 AAS27197	AAF18209 AAF89013	AAF89012	12	AAZ38124	AAL36156	AAS14155	AAV00641	AAZ94053	AAZ00365	AAF89027	AAZ00356	AAF89018	AAZ00352	AAF89010	AAZ38125	AAS91080	AAS85415	AAS91079	ABL12889	AAS83500	ABL12888	32	781	AAK75946	601	99	AAK09389	AAK35278	AA140995	327	AAI93426	184	AAS15727
22	22	22	20	20	22	22	19	21	20	22	20	22	20	22	20	23	23	23	23	23	23	22	22	22	22	22	22	22	22	24	22	20	23
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### ALIGNMENTS

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Stem loop; coconut foliar decay virus; CFDV; bacterial promoter; yeast promoter; tissue-specific; phloem-specific; CaMV 35S promoter; ss.
                                                                                                                                                         /*tag= b
/note= "Region binds to nucleotides 16 to 22"
                                                                                                                                                                                                                                   e
"Region binds to nucleotides 38 to 43"
                                                                                                                                                                                 CFDV-DNA fragment stem loop repeat region.
                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                        d
"RPT2"
        BP.
                                                                                                                                  /*tag= a
/note= "RPT1"
      AAX02689 standard; DNA; 44
                                      10-MAY-1999 (first entry)
                                                                                                 Coconut foliar decay virus
                                                                                                                                /*tag=
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27..32
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38..43
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/*tag=
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/*tag=
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                                                                                                                         stem_loop
                       AAX02689;
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AAX02689
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43"

/note= "Region binds to nucleotides 38 to

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misc_binding
                                                          21-JAN-1999
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                                                                                                                                                                                       This invention describes a coconut foliar decay virus (CFDV) DNA fragment that includes the stem-loop structure of CFDV DNA but lacks the translation start codons of open reading frames ORF1 and/Or ORF2. The new CFDV DNA fragment is useful as a bacterial or yeast promoter, as a promoter for tissue-specific (especially phloem-specific) gene expression in plants and for production of chimeric constructs for transient or stable expression. Certain fragments of CFDV DNA have stronger promoter activity in E. coli than the CaMV 35s promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stem loop; coconut foliar decay virus; CFDV; bacterial promoter;
yeast promoter; tissue-specific; phloem-specific; CaMV 35S promoter; ss.
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 /*tag= f
/note= "Region binds to nucleotides 27 to 32"
                                                                                                                                                 Coconut foliar decay virus promoters - for gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _{\rm r}^{\rm c} "Region binds to nucleotides 4 to 10"
                                                                                                                                                                                                                                                                                               100.0%; Score 22; DB 20; Length 44; 100.0%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                              Salamini F;
                                                                                               (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
                                                                                                                                                                                                                                                                       Sequence 44 BP; 8 A; 16 C; 17 G; 3 T; 0 other;
                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                CFDV-DNA fragment stem loop repeat region.
                                                                                                               Rohde W,
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                                                                                                                                                                            Disclosure; Fig 4; 14pp; German.
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                                                                                                                Randles JW,
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"RPT2"
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"RPT1"
                                                                                                                                                                                                                                                                                                                                                                                               AAX02687 standard; DNA; 44 BP
                                                              97DE-1030502
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                            DE19730502-A1
                                                                               16-JUL-1997;
                                                              16-JUL-1997;
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This invention describes a coconut foliar decay virus (CFDV) DNA fragment that includes the stem-loop structure of CFDV DNA but lacks the translation start codons of open reading frames ORF1 and/or ORF2. The new CFDV DNA fragment is useful as a bacterial or yeast promoter, as a promoter for tissue-specific (especially phloem-specific) gene expression in plants and for production of chimeric constructs for transient or stable expression. Certain fragments of CFDV DNA have stronger promoter activity in E. coli than the CaMV 355 promoter.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvolisant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidabetic; hypotensive; dermatological; immunosuppressive; antihilammatory;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Coconut foliar decay virus promoters – for gene expression in plants, bacteria and yeasts
                                                             /note= "Region binds to nucleotides 27 to 32"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 22; DB 20; Length 44; 100.0%; Pred. No. 18; tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Becker D, Hehn A, Randles JW, Rohde W, Salaminl F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 4; 12pp; German.
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Best Local Similarity 100.(
Matches 22; Conservative
38..43
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antiposotiatic; antiparkinsonian; nootropic; neuroprotective; costeopathic; antiponvulsant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coaqulant; vasotropic; timmunostimulant; cardiant; thrombolytic; coaqulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiabetic; hypotensive; dermatological; immunosuppressive; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, erythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, auttoimmune disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, concurrant invinities therapy antiminatory disease, to enhance complements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Secreted protein; human; gene therapy; diagnosis; treatment; cancer; protein therapy; tumor; neurodegenerative disorder; blood disorder; AIDS; developmental abnormality; leukemia; immune system; autoimmune disease; hepatic disease; renal disease; inflammation; allergy; schizophrenia; Alzheimer's disease; cognitive disorder; arthritis; infection; psoriasis; transplant rejection; diabetes; asthma; sepsis; acne; metabolic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids and peptides derived from open reading frame X, useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 324 BP; 82 A; 84 C; 89 G; 69 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted protein cDNA encoding gene 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 5; Page 1386-1387; 5507pp; English.
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                                                            31-MAR-2000; 2000WO-US08621.
                                                                                                        99US-0127607.
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                                                                                                                                                                                                            (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                 WPI; 2000-602362/57.
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Best Local Similarity
Than 20; Conserva
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                    05-OCT-2000,
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This invention describes novel human genes and the secreted proteins they encode. The polynucleotides and their corresponding secreted proteins they encode. The polynucleotides and their corresponding secreted polynucleotides are useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. Also pathological conditions can be diagnosed by determining the amount of the new polypeptides in a sample or by determining the presence of mutations in the new polynucleotides. Specific uses are described for each of the polynucleotides of the invention, based on which tissues they are most canned cancer, tumors, neurodegencrative disorders, developmental annormalities, blood disorders, leukemias, diseases of the immune system, autoimmune diseases, hepatic and an enal disease, inflammation, allergies, autoimmune diseases, hepatic and disease, inflammation, allergies, infections, AIDS, transplant rejection, diabetes, asthma, sepsis, acne, polymeptides or polymucleotides can also be used as food additives or inflammations. The polypeptides are also useful for identifying their which in arthers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                   Ni J;
                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated human genes, useful for diagnosis and treatment of, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human musculoskeletal system related polynucleotide SEQ ID NO 252.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            binding partners. AAZ27233-Z27265 encode human secreted proteins described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                 Yu G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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cardiovascular disorder; food additive; preservative; ss.
                                                                                                                                                                                                                                                                                                                               Rosen CA, Florence C, Young PE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1592 BP; 432 A; 382 C; 418 G; 360 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1066 CTGCCCAGGCCGGAGGCCTGAG 1045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAL34910 standard; cDNA; 313 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim la; 155; 306pp; English.
                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                           98US-0077687.
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                                                                                                                                                       99WO-US05721.
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                                                                                                                                                                                                                                                                                                                           Ruben SM, Ferrie AM,
                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-551363/46.
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                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB; AAY45265
                                         Homo sapiens.
                                                                                                                                                     11-MAR-1999;
                                                                                                                                                                                                           12-MAR-1998;
12-MAR-1998;
                                                                         WO9946289-A1
                                                                                                                                                                                         12-MAR-1998;
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                                                                                                                 16-SEP-1999
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Gaps

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29 - SEP - 2000; 2000US - 0.2368369.
29 - SEP - 2000; 2000US - 0.2368370.
02 - CCT - 2000; 2000US - 0.236802.
02 - CCT - 2000; 2000US - 0.236802.
02 - CCT - 2000; 2000US - 0.237039.
02 - CCT - 2000; 2000US - 0.237039.
02 - CCT - 2000; 2000US - 0.239935.
13 - CCT - 2000; 2000US - 0.239937.
20 - CCT - 2000; 2000US - 0.239937.
20 - CCT - 2000; 2000US - 0.241281.
20 - CCT - 2000; 2000US - 0.241786.
20 - CCT - 2000; 2000US - 0.241886.
20 - CCT - 2000; 2000US - 0.246475.
08 - NOV - 2000; 2000US - 0.246476.
08 - NOV - 2000; 2000US - 0.246477.
08 - NOV - 2000; 2000US - 0.246477.
08 - NOV - 2000; 2000US - 0.246524.
08 - NOV - 2000; 2000US - 0.246524.
08 - NOV - 2000; 2000US - 0.246527.
17 - NOV - 2000; 2000US - 0.246527.
17 - NOV - 2000; 2000US - 0.246513.
17 - NOV - 2000; 2000US - 0.246513.
17 - NOV - 2000; 2000US - 0.249210.
17 - NOV - 2000; 2000US - 0.249210.
17 - NOV - 2000; 2000US - 0.249211.
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17-NOV-2000; 2000US-0249244.
17-NOV-2000; 2000US-0249244.
17-NOV-2000; 2000US-0249265.
17-NOV-2000; 2000US-0249265.
17-NOV-2000; 2000US-0249297.
17-NOV-2000; 2000US-0249297.
17-NOV-2000; 2000US-0249297.
17-NOV-2000; 2000US-0249300.
01-DEC-2000; 2000US-0251030.
05-DEC-2000; 2000US-0251198.
05-DEC-2000; 2000US-0251198.
05-DEC-2000; 2000US-02511479.
06-DEC-2000; 2000US-02511479.
06-DEC-2000; 2000US-02511479.
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20000S-0251989.
20000S-0251990.
20000S-0254097.
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2000US-0249216.
2000US-0249217.
2000US-0249218.
           2000US-0234998.
2000US-0235484.
2000US-0235834.
2000US-02363535.
2000US-0236367.
2000US-0236368.
                                             27-SEP-2000;
27-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
neurological disease; infection; human; secreted protein; musculoskeletal system; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-SEP-2000; 2000US-0229345.
05-SEP-2000; 2000US-0229513.
06-SEP-2000; 2000US-0229513.
06-SEP-2000; 2000US-0239438.
06-SEP-2000; 2000US-0231243.
08-SEP-2000; 2000US-0231244.
08-SEP-2000; 2000US-0231244.
08-SEP-2000; 2000US-0231244.
08-SEP-2000; 2000US-023198.
14-SEP-2000; 2000US-023298.
14-SEP-2000; 2000US-023298.
14-SEP-2000; 2000US-0232399.
14-SEP-2000; 2000US-0232399.
14-SEP-2000; 2000US-0232399.
14-SEP-2000; 2000US-0232399.
14-SEP-2000; 2000US-0232399.
14-SEP-2000; 2000US-0232399.
14-SEP-2000; 2000US-0233398.
14-SEP-2000; 2000US-0233398.
14-SEP-2000; 2000US-0233363.
14-SEP-2000; 2000US-0233363.
14-SEP-2000; 2000US-0233363.
                                                                                                                                                                                                                                                                         16 MAR-2000; 2000US-0198974; 17-MAR-2000; 2000US-0198076; 18-APR-2000; 2000US-0198076; 19-APR-2000; 2000US-0209467. 20-UN-2000; 2000US-0209467. 20-UN-2000; 2000US-0214886; 30-JUL-2000; 2000US-0216886; 11-JUL-2000; 2000US-0216880; 11-JUL-2000; 2000US-0216880; 11-JUL-2000; 2000US-0216880; 11-JUL-2000; 2000US-021899; 26-JUL-2000; 2000US-021899; 26-JUL-2000; 2000US-0222964; 14-AUG-2000; 2000US-0225214; 14-AUG-2000; 2000US-0225214; 14-AUG-2000; 2000US-0225214; 14-AUG-2000; 2000US-0225266; 14-AUG-2000; 2000US-0225266; 14-AUG-2000; 2000US-0225266; 14-AUG-2000; 2000US-0225275; 14-AUG-2000; 2000US-0225275; 14-AUG-2000; 2000US-0225276; 14-AUG-2000; 2000US-0225276; 14-AUG-2000; 2000US-0225276; 14-AUG-2000; 2000US-0225276; 12-AUG-2000; 2000US-0225868; 22-AUG-2000; 2000US-0228924; 01-SEP-2000; 2000US-0229343; 01-SEP-2000; 2000US-
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2000US-0186628.
2000US-0186350.
2000US-0186350.
2000US-019874.
2000US-0198123.
2000US-0198123.
2000US-02515.
2000US-020515.
2000US-0216880.
2000US-021687.
2000US-021687.
2000US-021687.
2000US-021687.
                                                                                                                                                                      17-JAN-2001; 2001WO-US01338
                                                                                               WO200155367-A1
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04-FEB-2000;
24-FEB-2000;
                                                             Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fatty acid transport protein; FATP; hFATP; cardiomyopathy; diabetes; long-chain fatty acid metabolism; obesity; human; ss.
                                                                                                                                                        Isolated polypeptide for treating, preventing and/ or prognosing disorders related to the musculoskeletal system including musculoskeletal cancers and also for testing and detection e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 313;
                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 252; 781pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 313 BP; 53 A; 90 C; 106 G; 62 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80.9%; Score 17.8; DB 22;
90.5%; Pred. No. 5.5e+02;
Live 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human FATP alternatively spliced sequence.
                                                                           Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAZ38123 standard; cDNA; 496 BP
                                    (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89 TGCCCAGGCAGAAGGCCAGGG 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 tgcccaggccgaaggcctggg 22
 05-JAN-2001; 2001US-0259678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98EP-0400823.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 90.5 hes 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (JANC ) JANSSEN PHARM NV. (UNIW ) UNIV WASHINGTON.
                                                                       Rosen CA, Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             parasitic infections.
                                                                                                        WPI; 2001-451937/48.
                                                                                                                         P-PSDB; ABB03328
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                                                                                                                                                                                                               diagnosis
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The invention provides a human fatty acid transport protein (hFATP).

hBATP is believed to be involved in the modulation long-chain fatty acid metabolism; the protein and polynuclectides therefore enable production of compositions comprising a component requiating (inhibiting or compositions comprising a component requiating (inhibiting or compositions comprising a component requiating (inhibiting or compositions to the hFATP gene useful therapeutically to alter intracellular or blood levels of long chain fatty acids. Such compounds are especially useful to treat conditions associated with deficient regulation (e.g. may comprise an inhibitor to treat cardiomyopathies or diabetes or an enhancer to treat obesity. The polynucleotides are also useful to screen compounds for their effects on hFATP expression, e.g. by measuring mRNA transcription in cells/cell extracts (e.g. liver cells) contacted with the compound and comparing with that in noncontacted with the compound and comparing with that in noncontacted cells. Sequences AMX38122-123 represent nucleotide sequence of adipose tissue. The present sequence represents an alternative spliced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vanin-I; glycosyl hydrolase; glucohydrolase;
N-acetylglucosamine 6-P deacetylase; diagnosis;
treatment; prevention; expression; disorder; carbohydrate; metabolism;
antagonist; reproductive disorder; cell proliferation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                           New human fatty acid transport protein, hFAIP, useful to screen for inhibitors or enhancers useful to regulate fatty acid metabolism \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; homologue; HHH-6; N-terminal asparagine amidohydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Corley NC, Guegler KJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human hydrolase homologue HHH-6 cDNA fragment 1514414F6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 496 BP; 56 A; 151 C; 202 G; 87 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                      Auwerx J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lal P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                adipose tissue. The present sequence resequence found in the analyzed clones.
                                                                                                                                                    Claim 2; Fig 1A-D; 83pp; English.
                      Deeb SS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAZ49239 standard; cDNA; 524 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                435 TGCCCAGGCAGAAGGCCAGGG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 tgcccaggccgaaggcctggg 22
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Patterson C, Baughn MR;
                  Martin G, Nemoto M,
                                                         WPI; 1999-620202/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 19; Conserv
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Claim 27; Seq ID No 7879; 511pp; English.
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Best Local Similarity
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         coquences AAZ49235, AAZ49239, AAZ49242 and AAZ49259 represent human hydrolase homologue HHH-6 cDNA fragments. The full-length cDNA sequence is given in AAZ49228. Nucleic acids encoding HHH-6 cDNA sequence is given in AAZ49228. Nucleic acids encoding HHH-6 were initially identified in a uterine endometrium tissue cDNA covery HHH-6 has homology to NacetyJqlucosamine 6-p deacetylase. The invention relates to human hydrolase have homologues HHH-1 to HHH-7 (AAY58165-Y5817) which respectively have homology to N-terminal asparagine amidohydrolase, vanin-1, glycosyl hydrolases, glucohydrolase and N-acetyJglucosamine 6-p deacetylase. Such homologues are useful in methods for diagnosing, treating or preventing disorders associated with expression of hydrolases. The hydrolase homologues are useful for treating or preventing a carbohydrate metabolism disorder. Antagonists of these hydrolases can be used to treat or prevent a reproductive or cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pseudomonas aeruginosa DNA for cellular proliferation protein #373.
            New human hydrolase homologues, useful for treating or preventing a
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                                                                                                                                                                                                                                                                                                                                                                                                                                      80.9%; Score 17.8; DB 21; Length 524; 90.5%; Pred. No. 5.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antisense; ds; prokaryotic cellular proliferation gene; antibiotic; antibacterial; drug design.
                                                                                                                                                                                                                                                                                                                                                                                    Sequence 524 BP; 95 A; 160 C; 167 G; 90 T; 12 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                  Disclosure; Page 77; 91pp; English.
                             carbohydrate metabolism disorder
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26-MAY-2000; 2000US-20757P.
23-CCT-2000; 2000US-242578P.
27-NOV-2000; 2000US-253625P.
22-DEC-2000; 2000US-257627
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Best Local Similarity 90.59
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ELIT-) ELITRA PHARM INC.
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                                                                                                                                                                                                                                                                                                                                                   proliferation disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamamoto RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-FEB-2001;
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes their use in the discovery of novel antibiotics, the essential comes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus almonella typhi, Klebsiella convention is also useful for the identification of potential new targets invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins can be used to screen compounds in rational drug discovery for programmes. The antisense nucleic acid sequence is also useful to screen corporate to the antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence encodes an essential prokaryotic cellular proliferation protein.

Converse the sequence data for this patent did not form part of the printed specification, but was obtained in electronic to the print of the printed specification.
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90.5%; Pred. No. 5.1e+02;
iive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ftp.wipo.int/pub/published_pct_sequences.
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Clary D;
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CC novel protein kinases have been identified as members of the tyrosine cor serine/threadine kinase (PTK and STK) families. The polynucleotides cor serine/threadine kinase (PTK and STK) families. The polynucleotides cording protein kinases and the polypeptides may be used in the encoding protein kinases and the polypeptides may be used in the inappropriate kinase expression. For example, they may be used to treat cancers (especially cancers of haematopoletic origin), cardiovascular cancers (especially cancers of haematopoletic origin), cardiovascular disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes), cancers (e.g. schizophrenia), neurodegenerative disorders (e.g. schizophrenia), neurodegenerative disorders (e.g. aschizophrenia), neurodegenerative disorders (e.g. disease), inflammatory disorders (e.g. infertility).

CC disorders (e.g. HIV) and reproductive disorders (e.g. infertility).

CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).

CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).

CC disease (e.g. HIV) bolypeptides may be used as antigens in the production kinase polypeptides may be used as antigens in the productive of antibodies against the protein kinases and in assays to identify as modulators of protein kinase expression and activity.
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                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human reproductive system related antigen cDNA SEQ ID NO: 1853.
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                                                                                                                                                                                                                 Sequence 834 BP; 229 A; 177 C; 209 G; 219 T; 0 other;
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2000US-0216880.
2000US-0217487.
2000US-0217496.
2000US-0218290.
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2000US-0180628.
2000US-0184664.
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2000US-0205515.
2000US-0209467.
2000US-0214886.
2000US-0215135.
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2000US-0224519.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer; gene therapy; ss.
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02 - MAR - 2000; 2
16 - MAR - 2000; 2
17 - MAR - 2000; 2
19 - MAY - 2000; 2
07 - JUN - 2000; 2
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30-JUN-2000;
07-JUL-2000;
07-JUL-2000;
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04-FEB-2000;
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2000US-0229345.
2000US-0229509.
2000US-0229513.
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2000US-0230438.
2000US-0231242.
2000US-0231243.
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2000US-0229287
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14 - AUG - 2000;
22 - AUG - 2000;
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01-SEP-2000;
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AAS27197/c ID AAS27197 standard; cDNA; 1092 BP

AAS27197;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition
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17. NOV - 2000; 20000S-0249213.
17. NOV - 2000; 20000S-0249213.
17. NOV - 2000; 20000S-0249214.
17. NOV - 2000; 20000S-0249216.
17. NOV - 2000; 20000S-0249217.
17. NOV - 2000; 20000S-0249218.
17. NOV - 2000; 20000S-0249244.
17. NOV - 2000; 20000S-0249245.
17. NOV - 2000; 20000S-0249264.
17. NOV - 2000; 20000S-0249265.
17. NOV - 2000; 20000S-0249297.
17. NOV - 2000; 20000S-02492997.
17. NOV - 2000; 20000S-0249299.
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Neuroprotective; cytostatic; dermatological; immunosuppressive; tumour; antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer; immune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder; sickle cell anaemia; hyperproliferative disorder; Gaucher's disease; neurodegenerative disorder; Alzheimer's disease; Parkinson's disease; chromosomal abnormality; Down syndrome; ischaemia; renal disorder; cardiovascular; respiratory; wound healing; endocrine; Addison's disease; reproductive system; gastrointestinal; liver disorder; AIDS; ss; acquired immune deficiency syndrome.
                                                        cDNA encoding novel signal transduction pathway protein, Seq ID 232.
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2000US-0184664.
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14-AUG-2000;
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The invention relates to novel isolated polypeptides (I), and the invention relates to novel isolated polypeptides (I), and the antibody to (I) are useful for diagnosing, preventing and treating diseases including immune system disorders (e.g. congenital and acquired immunodeficiencies, autoimmune disorders (e.g. rheumatoid arthrits), inflammatory conditions, organ trapplant respections and graft versus host disease, infectious diseases (e.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and other blood-related disorders (isolated disorders), neurodegenerative disorders (e.g. daucher's disease and cancer), neurodegenerative disorders (e.g. daucher's disease, Parkinson's disease), chromosomal abnormalities (Down syndrome), isohaemic injury (e.g. stroke), renal disorders (e.g. glomerulonephritis), cardiovascular disorders (e.g. arrhythmia), respiratory disorders, dermatological disorders; in wound healing, epithelial cell proliferation, endocrine disorders; in Addison's disease), reproductive system disorders (cirrhosis), as stimulators of B-cell responsiveness to pathogens, activators of as stimulators of B-cell responsiveness to pathogens, activators of T-cells, to induce higher affinity antibodies, and as a means to induce tumour proliferation in pathologies e.g. acquired immune deficiency syndrome (AIDS). AAS26976-AAS27850 represent novel signal transduction axx
                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune
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ID AAF18209 standard; DNA; 1658 BP.
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Best Local Similarity 90.55
Matches 19; Conservative
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                                                                      cardioactive; immunomodulatory; muscular active; vulnerary; sastrointestinal; nephrotropic; antlinfective; gynecological; antibacterial; diagnosis; neural disorder; immune disorder; reproductive; proliferative disorder; wound healing; infectious disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer associated proteins represented in AAB58106 - AAB58548. Lung cancer associated proteins and polynucleotide sequences, their agonists, and antagonists may have neuroprotective; cytostatic; cardioactive; lummunomodulatory; muscular active general; vulnerary; gastrointestinal activity. The invention antiinfective; gynecological; or antibacterial activity. The invention also includes antibodies specific for the protein or polynucleotide sequences. The lung cancer associated polynucleotide sequences may be used for detection of lung cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The proteins may be used to treat disorders such as neural, immune, muscular, reproductive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds and infectious diseases. Polynucleotide sequences AAF18425 - AAF18433 and peptide AAB58499 are used in the course of the invention for the identification and characterisation of the polynucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lung cancer associated gene sequences, referred to as lung cancer antigens, useful for treatment, prevention, and diagnosis of disorders
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                                                  Human; lung cancer associated protein; neuroprotective; cytostatic;
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  Lung cancer associated polynucleotide sequence SEQ ID 228.
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Best Local Similarity 90.5
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acid transport proteins (FATPS) from a number of species, including FATP1, FATP2, FATP3, FATP3 and FATP6 from the human, FATP1-FATP5 from the mouse, FATP3 and brown c. elegans, and FATP from Aspergillus nidulans, Drosophila, zebrafish, Magnaporthe grisea, Mycobacterium tuberculosis and Cochliobolus heterostrophus. The FATP from M. tuberculosis and Cochliobolus heterostrophus. The FATP from M. tuberculosis can be used to identify inhibitors which can then be used to used to develop anti-fungal agents capable of preventing infection of tice. Those from the human can be used to develop treatments for diabetes, heart disease, obesity, hyperlipidaemia and weight control. The present sequence is one of the sequences described in the exemplification
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Fatty acid transport protein; FATP; human; mouse; rat; rice blast fungus; yeast; fat absorption; obesity; diabetes; heart disease; hyperlipidaemia; weight control; tuberculosis; TB; anti-fungal; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present invention provides the protein and coding sequences of fatty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New fatty acid transport proteins (FATPs) useful for the manufacture of medicament for treating obesity, diabetes and heart disease -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tartaglia LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1938 BP; 349 A; 571 C; 615 G; 403 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stahl A, Hirsch DJ, Lodish HF, Gimeno RE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human FATP1 coding sequence SEQ ID NO: 28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 30; 287pp; English.
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ID AAF89012 standard; DNA; 1941 BP.
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                                                                                                                                                                                                                                                                                                                                                                                     99US-0405504
                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0465280.
                                                                                                                                                                                                                                                                                                                        21-SEP-2000; 2000WO-US25891
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19; Conserv
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                                                                                                                                       Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-FEB-2000;
06-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                           23-SEP-1999;
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The present invention provides the protein and coding sequences of fatty acid transport proteins (FATPS) from a number of species, including FATP1, FATP2, FATP4, FATP5 and FATP6 from the human, FATP1-FATP5 from the mouse, FATPa and b from c. elegans, and FATP from Aspergillus nidulans, Drosophila, zebrafish, Magnaporthe grisea, Mycobacterium tuberculosis and cochliobolus heterostrophus. The FATP from M. tuberculosis can be used to identify inhibitors which can then be used to tase to the fath of the from M. grisea (also known as rice blast fungus) can be used to develop anti-fungal agents capable of preventing infection of rice. Those from the human can be used to develop treatments for diabetes, heart disease, obesity, hyperilpidaemia and weight control. The present sequence is one of the sequences described in the exemplification
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                                                                                                                                                                                                                                                                            New fatty acid transport proteins (FATPs) useful for the manufacture of medicament for treating obesity, diabetes and heart disease -
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                                                                                                                                                                                                                  Lodish HF, Gimeno RE, Tartaglia LA;
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0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1941 BP; 325 A; 620 C; 651 G; 345 T; 0 other;
                                                                                                                                                                    (WHED ) WHITEHEAD INST BIOMEDICAL RES.
                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 30; 287pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human FATP protein encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAZ38122 standard; cDNA; 2219 BP.
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                                           21-SEP-2000; 2000WO-US25891.
                                                                                                                                                                                   (MILL-) MILLENNIUM PHARM INC
                                                                                                         99US-0465280.
2000US-0506252.
                                                                             99US-0405504.
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Best Local Similarity 90.59
Matches 19; Conservative
                                                                                                                                                                                                                Stahl A, Hirsch DJ,
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                                                                                                                       17-FEB-2000;
06-JUL-2000;
                                                                                          23-SEP-1999;
16-DEC-1999;
                29-MAR-2001.
                                                                           23-SEP-1999;
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The invention provides a human fatty acid transport protein (hFATP).

The invention provides a human fatty acid transport protein (hFATP).

The provides is believed to be involved in the modulation long-chain fatty acid metabolism; the protein and polynocleotides therefore enable production of compositions comprising a component regulating (inhibiting or compositions comprising a component regulating (inhibiting or later acid intracellular or blood levels of long chain fatty acids. Such compounds are especially useful to treat conditions associated with deficient regulation (e.g. may comprise an inhibitor to treat cardiomyopathies or diabetes or an enhancer to treat obesity. The polynucleotides are also useful to screen compounds for their effects on heATP expression, e.g. by measuring mRNA transcription in cells/cell extracts (e.g. liver calls) contacted with the compound and comparing with that in non-contacted with the compound and comparing with that in non-contacted cells. Sequences AAZ38122-123 represent nucleotide sequence of adipose tissue. The present sequence represents a cDNA library of human human human manners.
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                                                                                                                                                                                                                                                                                                                                                                                             New human fatty acid transport protein, hFATP, useful to screen for inhibitors or enhancers useful to regulate fatty acid metabolism -
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                                                                                                                     Deeb SS, Auwerx J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 2; Fig 1A-D; 83pp; English.
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                                                                                                              Martin G, Nemoto M,
                                                                                                                                                                                                                             WPI; 1999-620202/53
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Search completed: June 19, 2002, 16:50:44 Job time: 17502 sec

Fatty acid transport protein; FATP; hFATP; cardiomyopathy; diabetes; long-chain fatty acid metabolism; obesity; human; ss.

99WO-EP02295. 98EP-0400823.

W09951740-A2

14-OCT-1999.

(JANC ) JANSSEN PHARM NV

06-APR-1998;

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